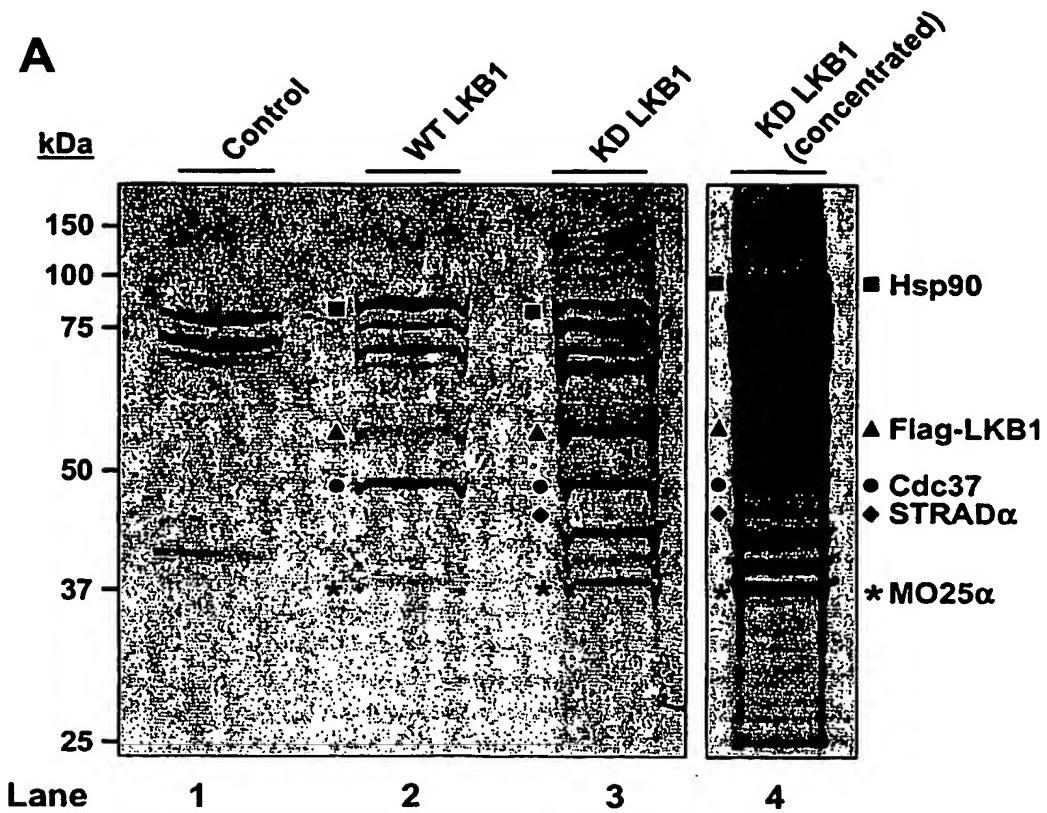


Figure 1

BEST AVAILABLE COPY

Figure 1a**B**

	Protein name	Peptide matches	% sequence coverage	NCBI gi number
■	Hsp90	15/44	30%	20149594
▲	Flag-LKB1	14/46	35%	7106425
●	Cdc37	31/72	59%	5901922
◆	STRAD α	11/80	34%	12060855
*	MO25 α	17/37	47%	7706481

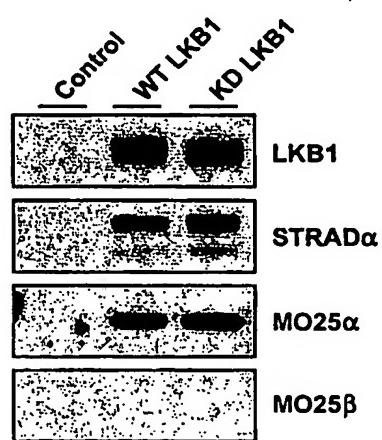
C

Figure 2**A**

hMO25α	1	MIF-PFGKSHKSPADIVKNCRESKAKLRRD-	-I	SDKKAERAKATEEVSKNLVA
hMO25β	1	MPL-PSKSHKSPADIVKNCRESKAKLRRD-	-D	DKKTEKASEEVSKSLOA
dMO25	1	MPL-PGKSHKSPADIVKNCRESKAKLRRD-	-D	DKKTEKASEEVSKSLOA
cMO25α	1	WLKPFLCKWDDKTPADIVKNCRESKAKLRRD-	-TNTSE	KVEKAERDTAKMIAL
cMO25β	1	WLKPFLCKWDDKTPADIVKNCRESKAKLRRD-	-TNTSE	KVEKAERDTAKMIAL
				SDKKYEVSKNLVA
hMO25α	50	MKEETLYGL-NEKEP-QTEAVAAQLAQELYNSGGLSTLADQLIDFEGKKDVQIENNL		
hMO25β	46	MKEETLYGL-NEKEP-QTEAVAAQLAQELYNSGGLSTLADQLIDFEGKKDVQIENNL		
dMO25	46	MKEETLYGL-SIAEPPADYVVAQLEQELYNSGGLSTLADQLIDFEGKKDVQIENNL		
cMO25α	53	AKTFREYGEDANEPNN-BQVOLAAQEVNLYVPLIKHHRFEFECKKDVAQEFNNNL		
cMO25β	60	TKSFITYQNDSAEPPSEHVVQVAQLAQELYNSGGLSTLADQLIDFEGKKDVQIENNL		
hMO25α	107	RHQIGTRSPPTVEYICTOONIIFMLLKGYH-SPEIALRCCMLRECIRHEPLAKIILNS		
hMO25β	103	RHQIGTRSPPTVEYISWPHIFMLLKGYH-APOIALRCCMLRECIRHEPLAKIILNS		
dMO25	104	RHQIGTRSPPTVEYICTKPEIIFTIASYEDAHPHIALNSCMLRECARYPLAKIILNS		
cMO25α	110	RHQIGTRSPPTVEYIAAPPEIIFTLLGYH-OPIIAALCCMLRECIRHEPLAKIILNS		
cMO25β	120	RHQIGTRSPPTVEYAGAPPEIIFTLGYSV-VPHIAALCCMLRESIRHPLAKIILNS		
hMO25α	165	QFDFFYVEMSTFDIASDAFTFKDILLTRHKIISAEFLKQHYDFPF-SEVERLLHSENY		
hMO25β	161	QFDFFYVEMSTFDIASDAFTFKDILLTRHKIIVAFLEQVDTIFF-EDVERLLHSENY		
dMO25	164	EFDKFFYVEMSTFDIASDAFTFKDILLTRHKIISAEFLDANYDFPSQHNQALLNSENY		
cMO25α	168	YFORFFYEVTSDFVFDIASDAFTFKDILTRHKIISAEFLDHYDFPF-GQXALTNSENY		
cMO25β	176	VFTYFFYEVSEVDIESDAFTFKDILTRHKIISAEFLDSHYDFPF-ACYONULLNSKJY		
hMO25α	224	VTKRQSLKLLGELLLDRHNFMTKYISOPENLKLMMNLLRDKSRNIQFEAFHVFKVFVA		
hMO25β	220	VTKRQSLKLLGELLLDRHNFMTKYISOPENLKLMMNLLRDKSRNIQFEAFHVFKVFVA		
dMO25	224	VTRRQSLKLLGELLLDRHNFMTKYISOPENLKLMMNLLRDKSRNIQFEAFHVFKVFVA		
cMO25α	227	VTRRQSLKLLGELLLDRHNFMTKYISOPENLKLMMNLLRDKSRNIQFEAFHVFKVFVA		
cMO25β	237	VTRRQSLKLLGELLLDRHNFMTKYISOPENLKLMMNLLRDKSRNIQFEAFHVFKVFVA		
hMO25α	284	NPNKTOPIDILLRNQAKLLEELFLSKPQNDEPTEDEQFNDEKAYLQKIQIILKRPQQEA--		
hMO25β	280	SPHKTOPIDILLRNQAKLLEELFLSKPQNDEPTEDEQFNDEKAYLQKIQIILKRPQQEA--		
dMO25	284	NPNKPKPIDIILLRNQAKLLEELFLSKPQNDEPTEDEQFNDEKAYLQKIQIILKRPQQEA--		
cMO25α	287	NPNKPKPIDIILLRNQAKLLEELFLSKPQNDEPTEDEQFNDEKAYLQKIQIILKRPQQEA--		
cMO25β	297	NPNKPKPIDIILLRNQAKLLEELFLSKPQNDEPTEDEQFNDEKAYLQKIQIILKRPQQEA--		
hMO25α		-----		
hMO25β		-----		
dMO25		-----		
cMO25α		-----		
cMO25β	357	KSKEDEDNQEPAAGPSEGPTSQ		

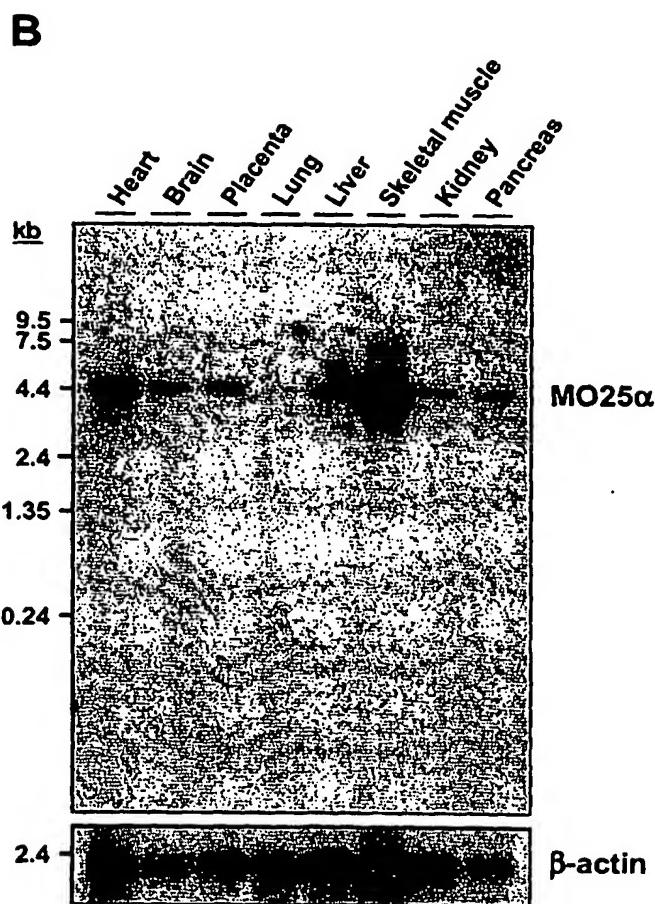
Figure 2a

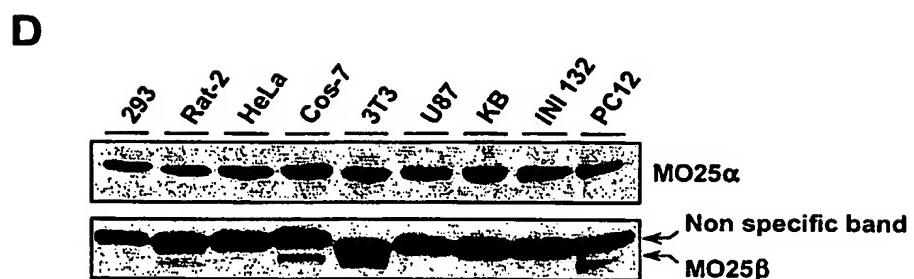
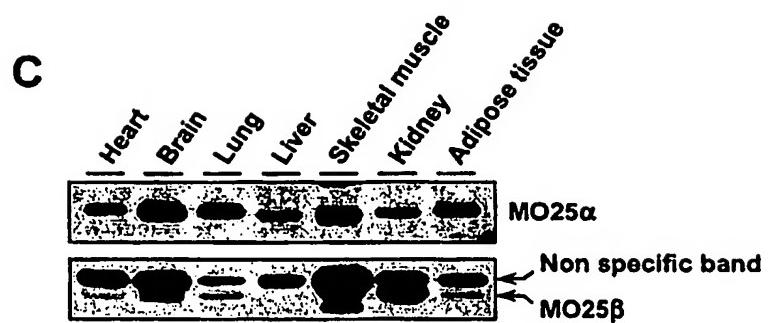
Figure 2b

Figure 3

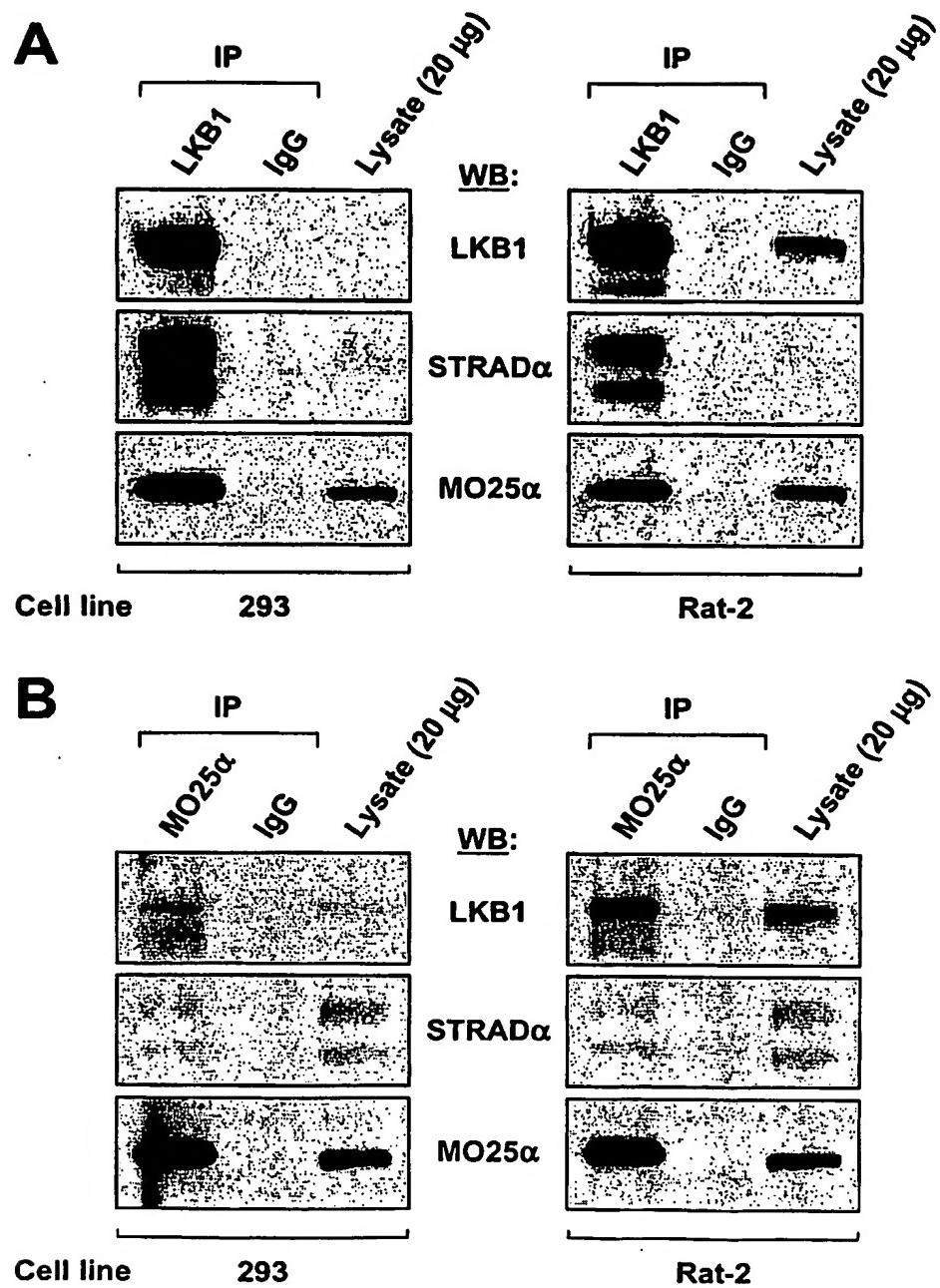


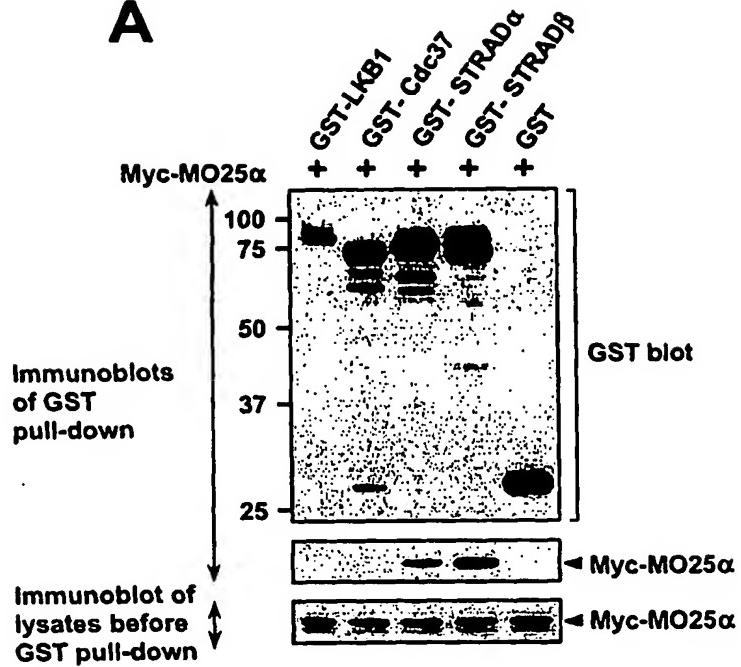
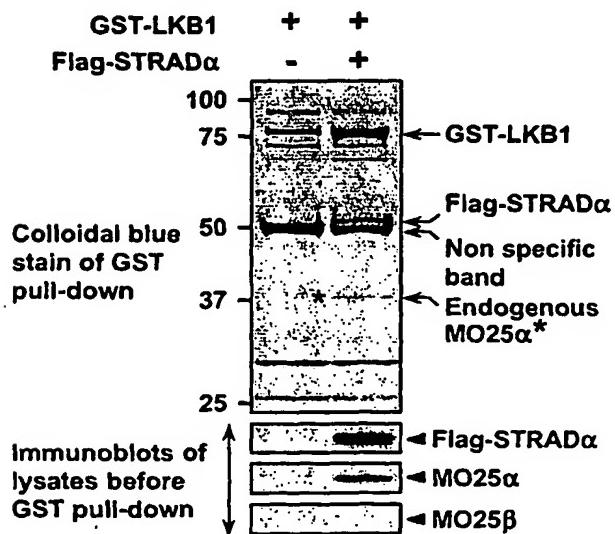
Figure 4**A****B**

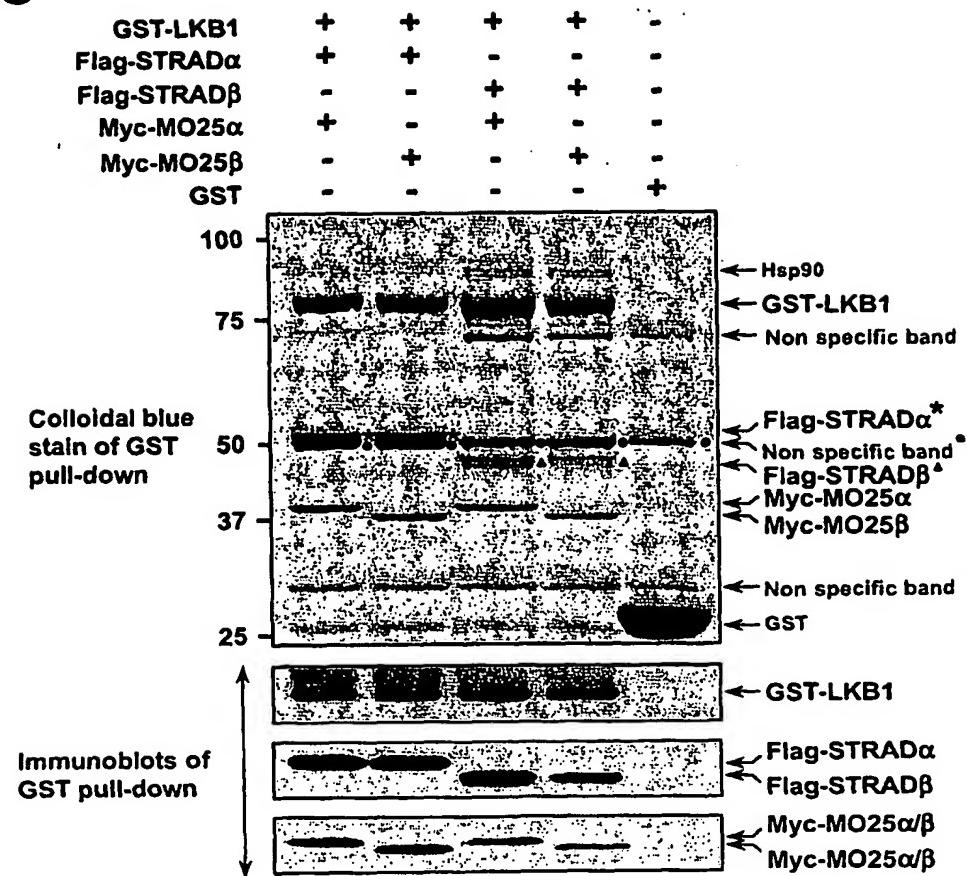
Figure 4a**C**

Figure 5

	MO25α	STRADα	LKB1
MO25α	A	B	C
STRADα	D	E	F
MO25α + STRADα	G	H	I

Figure 5a

	J	K	L
LKB1			
STRAD α + LKB1	M	N	O
MO25 α + STRAD α + LKB1	P	Q	R

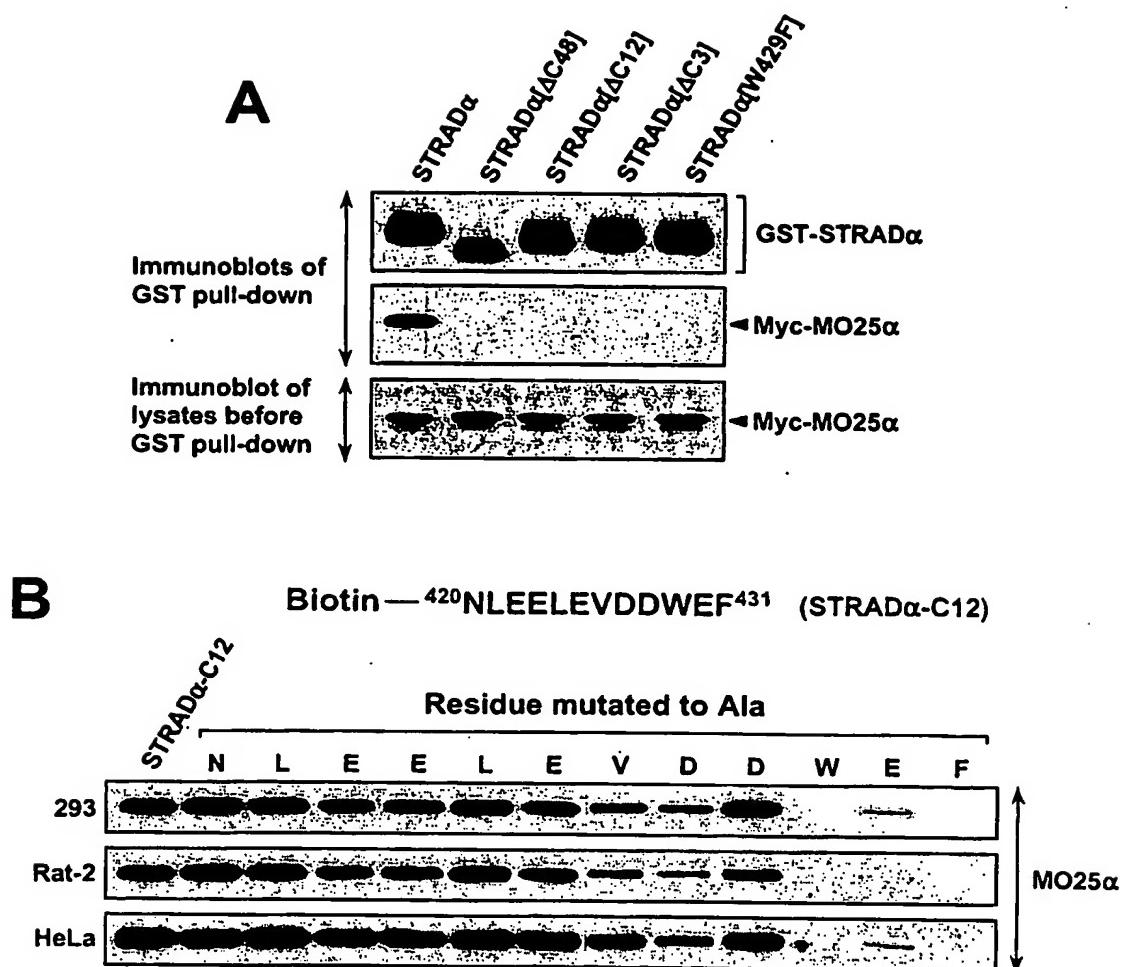
Figure 6

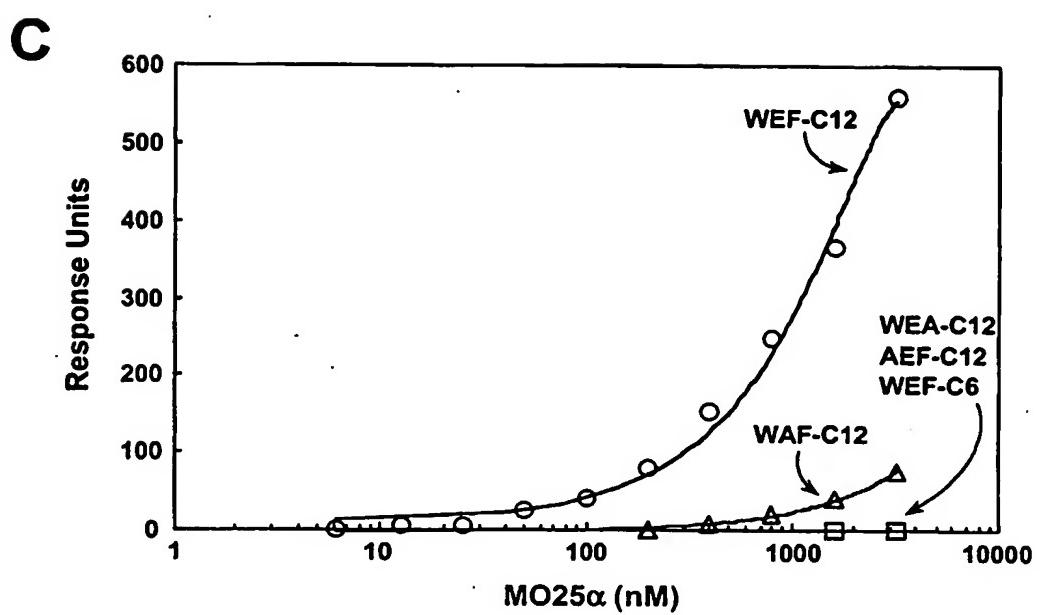
Figure 6a

Figure 7

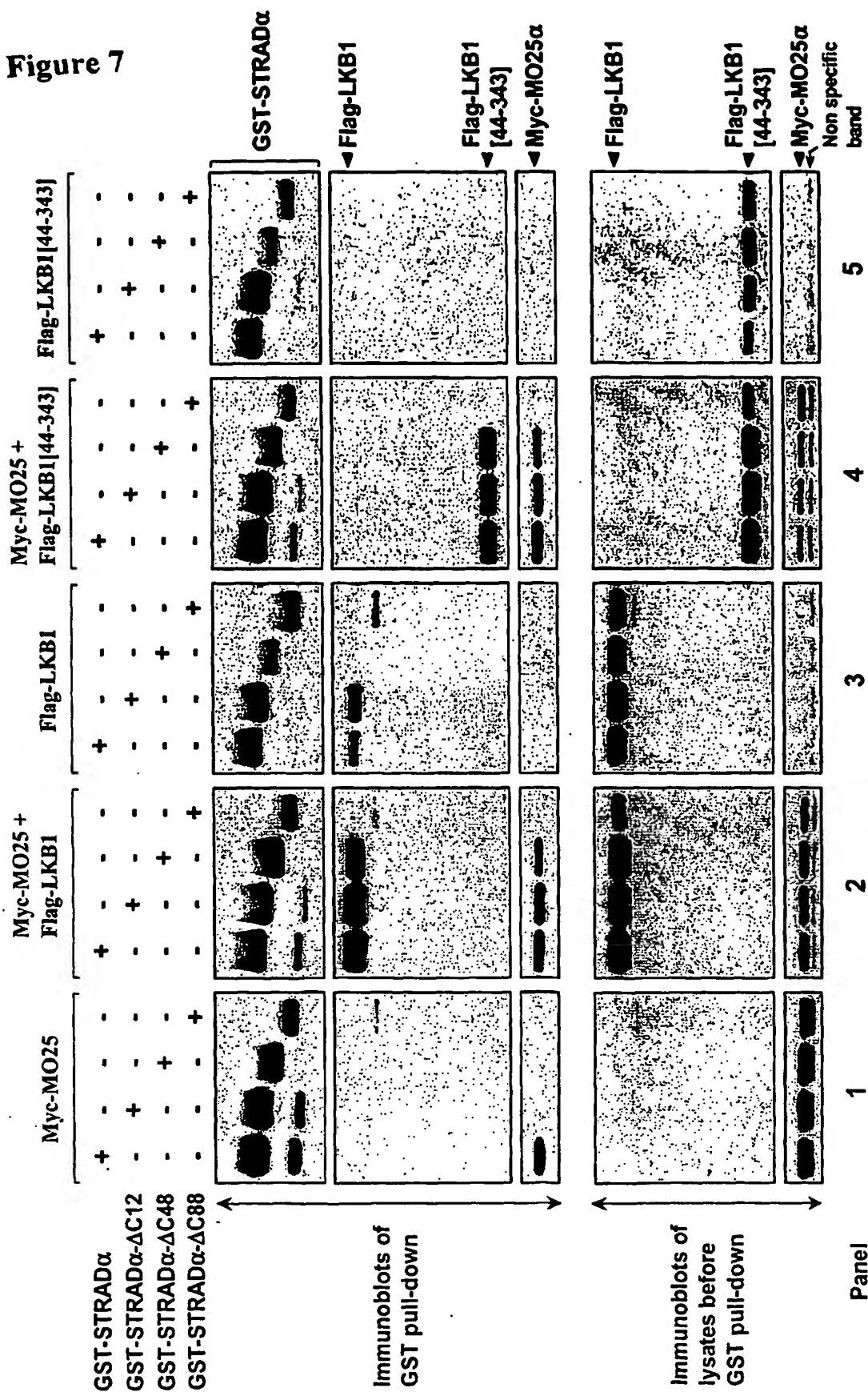


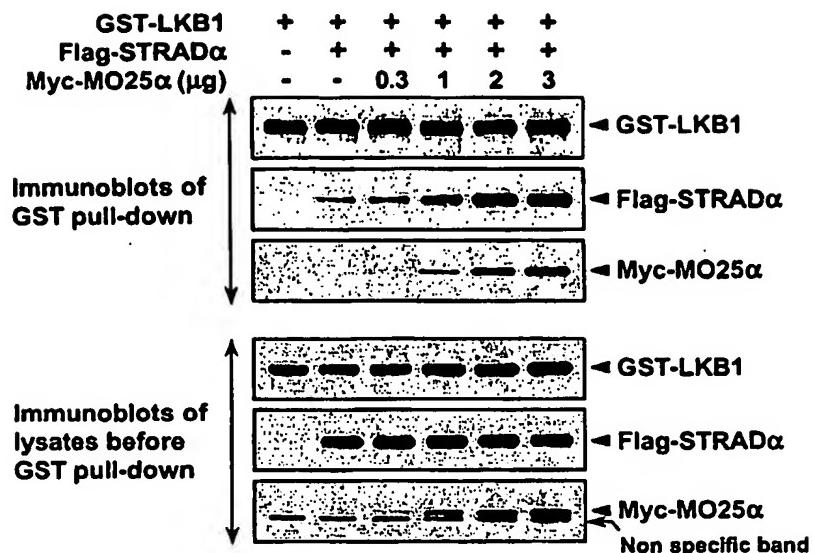
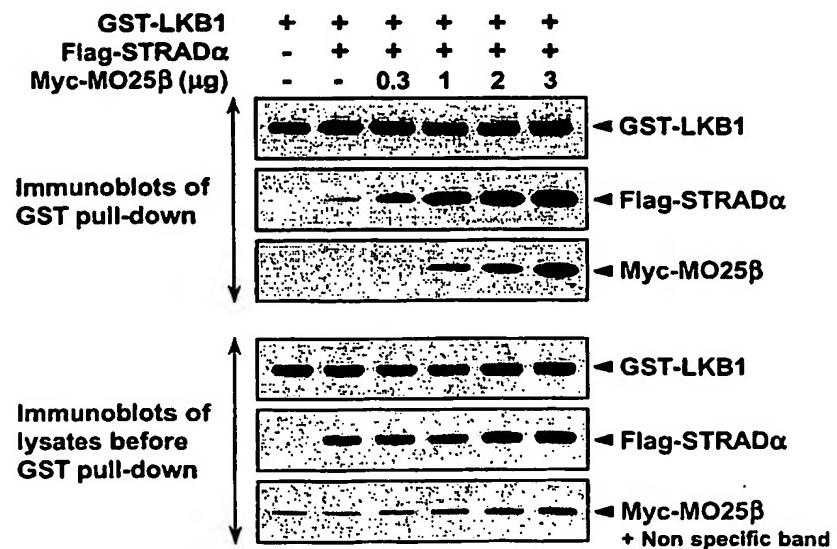
Figure 8**A****B**

Figure 9

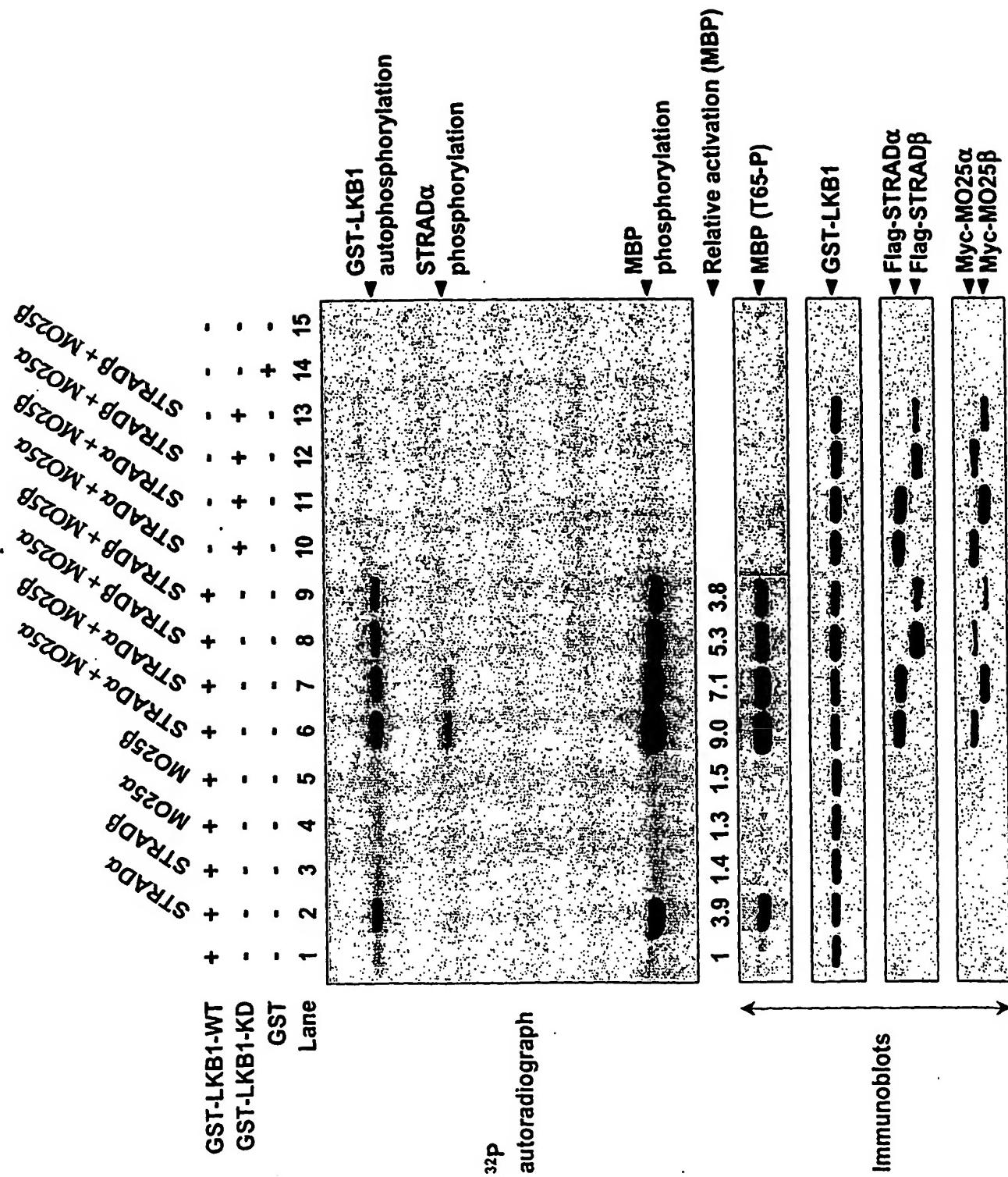


Figure 10

hSTRADAα	1 MSFLAVSKLIERIRRHVSEK FWK IVEGIRDLELFGEPPGDTNRKTNDASSEIASF KQEVMS
hSTRADβ	1 -----MELIDOPCTISHTDVSLEPEK----- GSEUSIEQYLVDEPIILWSRIPSTRAEV
hSPAK	1 -----MAEPGSPVH W OLPODAAP Y TAAAAA A APAPA A APAPA A APAPA A AV M ED Q AD
hOSR1	1 -----
hSTRADAα	61 SELPEGGCYELTVIGKGFDLMTVHLARYKPTGEYVT V RRI N I E AGSNE H VT F LOGE H
hSTRADβ	50 LOSTNVSHYEI Q VE I GRGF D NLT S VHLARH T PTGL T V I INLEN C NEERLK A QAVI
hSPAK	57 GMPIC C DAYE I QEV I GSG----- ATAVVQAA LCKPRO R V A I K R I N L E K COT S MD L L K -EIQ
hOSR1	9 PW S INR D DY E LO E V I GSG----- ATAVVQAA YCAPKK E V A I K R I N L E K COT S MD L L K -EIQ
hSTRADAα	121 VSKLFNRPNIVPYRAT I F J ADNELEM T SP M AYGS A K D I C THFMDG----- F NELA T AY
hSTRADβ	110 LSHFFRHPN I TTY H TV F VG S W I W I SP M AYGS A SQL R TYF P E G ----- M SE F FR R N
hSPAK	114 AMSQC S RPN M V T YYT S F V V K DEL A I V MR L LSGGSM H DE B I K Y I VNRGEH K NGV L EEA L IA T
hOSR1	66 AMSQC S RPN I V E YYT S F V V K DEL A I V MR L LSGGSM H DE B I K Y I VAKGEH K SG E TEST I AT
hSTRADAα	175 I L OQ G V L K A LDY G H H M G V H E S V K A S H I I L S V D G K V Y I I S GL R S N L M I S H C Q R Q R V U H D P F
hSTRADβ	164 I L FG A V R G L N Y L H Q G C H R S T K A S H I I L S G D G L V I H S G L S H S I V K H Q R R H A V Y D P F
hSPAK	174 I L M B V L E G L D L H R N Q I I H R D I K A G N I I L G E D G S V Q I A D F G V S A F L A T G D V I T R -- N K V R
hOSR1	126 I L IP E V L E G L E Y L H I Q G Q I I H R D V K A G N I I L G E D G S V Q I A D F G V S A F L A T G D I T R -- N K V R
hSTRADAα	235 KYSVKLP E ILS P E V I Q Q N Q O GYDA K SDIMSV G IT A CEL A NC H V P K D PA T OM I DE K LG N
hSTRADβ	224 QF S TSV Q W N S P E I A R ODL H GY I V K S D IMSV G IT A CEL A SG Q V P QDM H R T Q L Q K L K G
hSPAK	232 KTFV G TC C W M MA P E V MEQ - VR G YDF K AD I NS F GI T AE L AT G A P H K Y P PM K V L LT I QN
hOSR1	184 KTFV G TC C W M MA P E V MEQ - VR G YDF K AD I NS F GI T AE L AT G A P H K Y P PM K V L LT I QN
hSTRADAα	295 -----T V P-----CLL-DT S T I P A E E L T MS P SR S V A N G L-S D SL
hSTRADβ	284 -----PP Y SP-----L--DI S I P Q E S R M K N-S Q SG V D S G I G S V L
hSPAK	291 DP P T L E T GV E D K E M K K Y G K S FR K I H I L SC L Q K D P S K R P T A E L L K C K E F Q O K A K N R - E M I H
hOSR1	243 DPP S LET G V Q D K E M K K Y G K S FR K I H I L SC L Q K D P S K R P T A E L L K H K E F Q O K A K N K - E F L Q
hSTRADAα	328 TT S T P PS N G W P S E P Y H R T --FSP P H F H F V E Q C L Q R N P D ARP S A S T L LN H S F K Q I K R R
hSTRADβ	318 VSSG T I H TV N SD R L H TP S SK T --FSP A F S L V Q L C I QQ D P E K R P S A S L L SH V FF K OM K E E
hSPAK	350 E K L L TR T P D I A Q R A K K V R R V P G S S C H L H K T E D G W E W S D D E K S H E G K A F S Q E K S R R
hOSR1	302 E K I L Q R A P T I S E R A K V R R V P G S S C G L H K T E D G W E W S D D E E S E G K A A I S Q L R S R R
hSTRADAα	386 ASK-----A I P R I L RP-----V T P I T N E
hSTRADβ	376 S Q D-----S I L S LL P
hSPAK	410 V K E -- E N P E H A V S S - -----I I P B O H QS-----I I S M H D S Q G P P N A N E D Y
hOSR1	362 VK E S I S N S E L F P I T D P V G T L L Q V P E O I S A H L P Q A G Q I A T Q P T Q V S L P T A E P A K T A Q A L
hSTRADAα	404 E G S Q -S-----QDH S G T F G L V T N L E E L V D D W F-----
hSTRADβ	389 N K P S I S -----L P P V L P W T E P C D F P D E K D S Y W E F-----
hSPAK	447 R E F S -S-----C A V N L V L R L R N S R K E L N D I R F-----E F T P G R D T A E G V S Q E L F S A G L V D G E D V I
hOSR1	422 S G G S S Q E T K I P E S L V L R R N S R K E L N D I R F-----E F T P G R D T A E G V S Q E L F S A G L V D G E D V I
hSTRADAα	502 VAANLOKI V D E P K A L K T L T F K L A S G G D G S E I P D E V K L I G F A Q L S M
hSTRADβ	482 VAANLOKI V E E P Q S N R S V T F K L A S G V E G S D I P D D G K L I G F A Q L S M

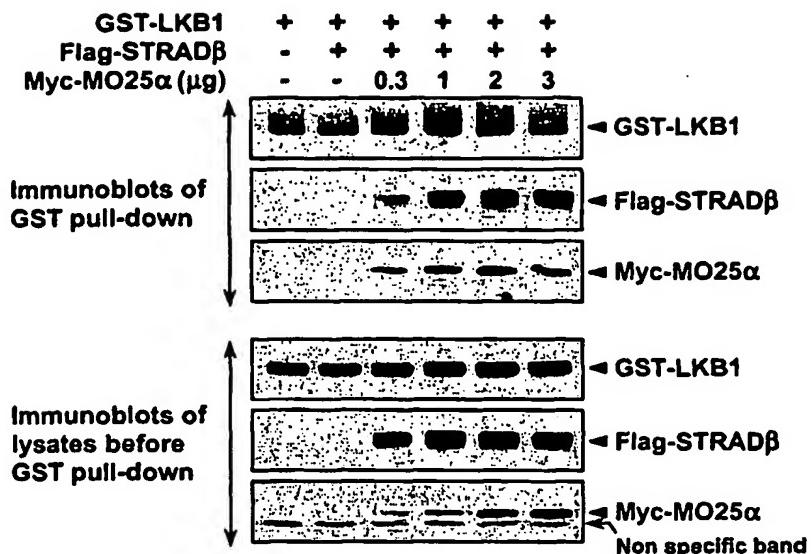
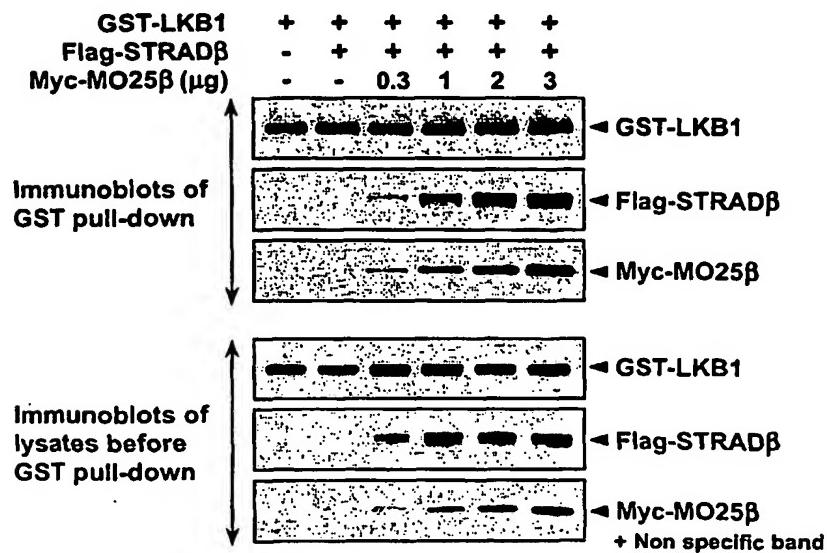
Figure 11**A****B**

Figure 12

Tos3	11	..LPRSSLLYNNASNNSRIKETRKVKLLYNPLTKR.....Q...ILNNFEILATLGNGQ
Pak1	94	..TPTTSSFCSSGSSKNKVETNRISLTYPVSKR.....K...VLNTYEIIKELGHGQ
CaMKK β	121	CICPSLPYSPVSSPQSSPRLPRTVESHVSITGM.....QDCVQLNQYTLKDEIGKGS
LKB1	7	QQLGMFTEGELMSVGMDTFIHRIDSTEVIYQP..RR.....KRAKLIGKYLMGDLLGEGS
Elm1	39	TSSFGSSFSQQKPTYSTIIGENIHTILDEIRPYVKKITVSDQDKKTINQYTLGVSAGSGQ
consensus	121	p ss s s ss rik tv l y pltkr q ilnnny i 1G Gq
Tos3	61	YGKVKLARDLGTGALVAIKILNRFKRS....GYSL.....QLKV.EN.....
Pak1	144	HGKVKLARDILSKQLVIAKIVDRHEKKQRKFTFIK.....SSKISEN.....
CaMKK β	176	YGVVKLAYNENDNTYYAMKVL SK..KKLIRQAGFPR.....RPPRGTRPAPGGCIQP
LKB1	60	YGKVKEVLDSETLCRRAVKILKK..KKLRR.....
Elm1	99	FGYVRKAYSSTLGKVVAVKIPKKPWNAQQYSVNQVMRQIQLWKSKGKITTNMSGNEAMR
consensus	181	yGkvkla d t lvAikil k kk k y k
Tos3	99	...PRVNQEIEVMKRCHHE.NVVELYEILNDPESTKVLVLEYCSRGPVKWCPENKMEI
Pak1	187	...DIKIREIAIMKKCHHK.HVVKQLEIVLDDLKSRKIYLVLEYCSRGEVKWCPPDCMES
CaMKK β	227	RGPIEQVYQEIAILKKLDHP.NVVKLVEVLDDPNEDHLYMVFELVNQGPV.....MEV
LKB1	89	PNGEANVKKEIQLLRLRHK.NVIQLVDVLYNEEKQKMYMVMEYC.....VCGMQEM.L
Elm1	159	LMNIEKCRWEIFAASRLRNNHVIRLIECLDSPFSESIWIVTNWCSLGELOQWKRDDDEDI
consensus	241	drvk EI vmkrlhh nvv LievLddp s kvylVleycs g v wc mei
Tos3	154	.KAVGPSILTFFQQ....SRKVVLDDVSGLEYLHSQGITHRDIKPSNLLISSNGTV.KISD
Pak1	242	.DAKGPSLLSFQE....TREILRGVVLGLEYLHYQGIIRDIKPSNLLISGDGTV.KISD
CaMKK β	279	.PTLKP..LSEDQ....ARFYFQDLIKIEYLHYQKIIIRDIKPSNLLVGEDGHI.KIAD
LKB1	141	.DSVPEKRFPVVCQ....AHGYFCQLIDGLEYLHSQGIVHKDIKPGNLLTTGGTL.KISD
Elm1	219	LPQWKKIVISNCVSVTFAKKILEDMTKGLLEYLHSQGCIHRDIKPSNILLDEEEKVAKLSD
consensus	301	v p ils q ar vv dvv GLEYLhsQgiiHrDIKPsNLLis dgtv KisD
Tos3	208	FG..VAM.STATGSTNIQSSHEQLLKSRALGTPAFFAPELCSTEKEY.....
Pak1	296	FG..VSIAASSTNSSDSESLSDELELAKTVGTPAFFAPEMCLGEDAFTRYNLTKENLFRG
CaMKK β	331	FG..V.....SNEFKGS..DALLSNTVGTPAFMAPESLS.....ETRKIFSG
LKB1	195	LG..VAEALHPFAADDTCRTSQ.....GSPAFQPPEIANGLDTFS.....
Elm1	279	FGSCIFTQSLPFSANFEDCFQRELNKIVGTPAFIAPELCHLGNSKRDFVTD.....
consensus	361	fG v t s d s 1 r vGtPAF aPElc y
Tos3	252	SC.SSAIDIWSLGVTIYCLLFGKLPFNANSGLELFDSIINKPLEFPSYEEMLNGATSGIT
Pak1	354	SCISFMIDIWAVGVTLYCLLFGMLPFFSDFELKLFKEIVNDPLKFPTFKEIQSNKVSKVS
CaMKK β	369	K....ALDVWAMGVTLYCFVFGQCPFMDERIMCLHSKIKSQALEFPDOPDIA.....
LKB1	233	...GFKVDIWSAGVTLYNITTGLYLPFEGDNIYKLHENIGKGSYAI.....
Elm1	332	...GFKLDIWSLGVTLYCLLYNELPFFGENEFETYHKIEEVSSLSSKINGNTLNDLVIKRL
consensus	421	f idIWslGVTLYcllfg 1PF ad 1 lfdkli 1 fp em
Tos3	311	M.EEYT...DAKDLKKLLQKDPDKRIKLAVIDKVFHPFMC.....HYGKSDAASVL...TN
Pak1	414	CEEEYE...MAKDLLLKLLEKNPQKRMTIPIAKKHPFVS.WDFDHVPENDEKLLS...SV
CaMKK β	417E...DLKDLITRMLDKNPESRIVVPEIKILHPWVTRHGAEPPLPSEDENCTLVEVTE
LKB1	276	.GDCGP...PLSDLKGMLEYEPAKRFSIIRQIROHSWFRK...KHPPAEAPVPIPSP PDT
Elm1	389	LEKDVTLRISIQLDVKVLSDQPIDSRNHSQISSSS.VNPVRNEGPVRRFFGRLLTKKGK
consensus	481	ee . 1kDlkklleknP kri 1 ik hpfv dh p d v1 t
Tos3	359	LETFHETKVSPP.....SSCKRVELVSLPVNSSFASLDSSVYMFHDHNNLRTGADRNS
Pak1	467	LE..QKLRF.....QCNQTDQFE.PISISKHELKNAV.....SGVGKKIKESV
CaMKK β	469	EEEVNSVKHIPSLATVILVKTMRKRSFGNPFEGRSREERSLSAPGNLLTKQGSEDNLQG
LKB1	329	KDRWRSMTVVPYLEDLHGADEDDEDLFDIEDDIITYQDFTVPGQVPEEEASHNGQRRGLPK
Elm1	448	KKTSGKGKDKVLVSATSKVTPSIHIDEEPDKECFSTTVLRSSPDSSDYCSSLGEAEIQVT
consensus	541	e 1k p l rve pv s lks s lg

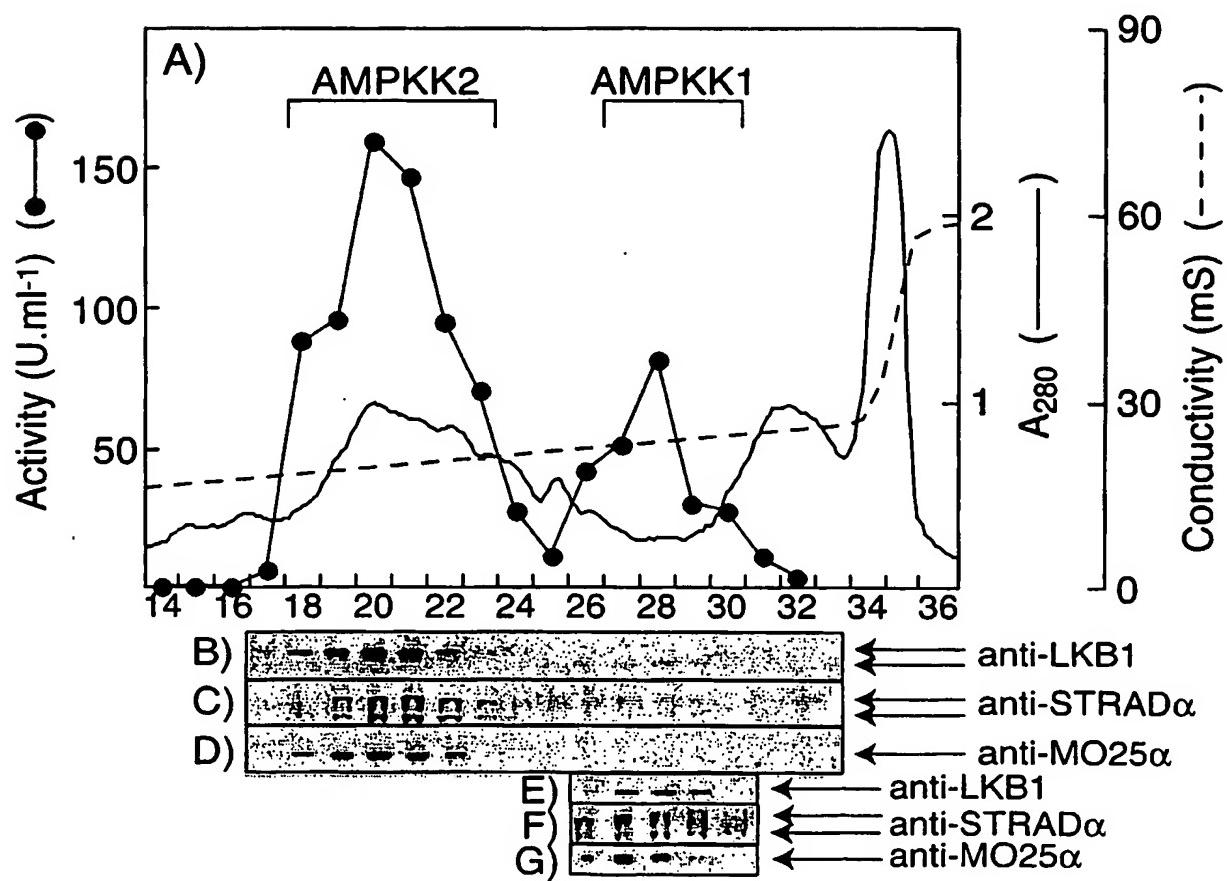
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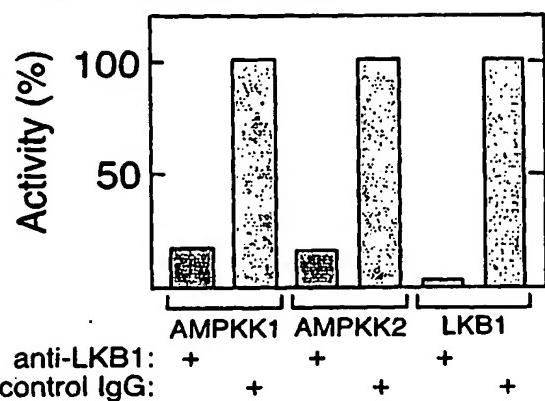
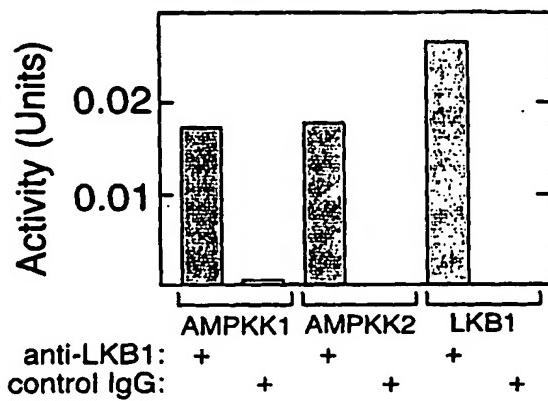
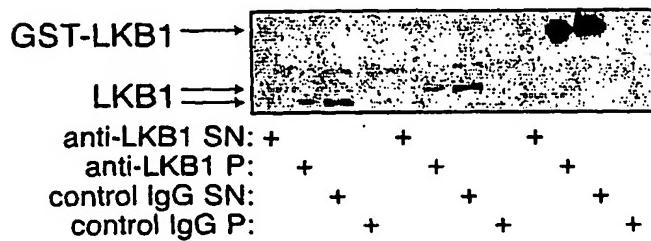
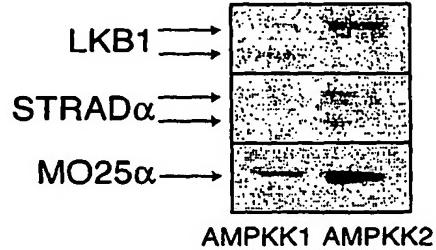
Figure 14**A) Activity in supernatant****C) Activity in pellet****B) Immunoprecipitation of polypeptides****D) Immunoblotting of pellets**

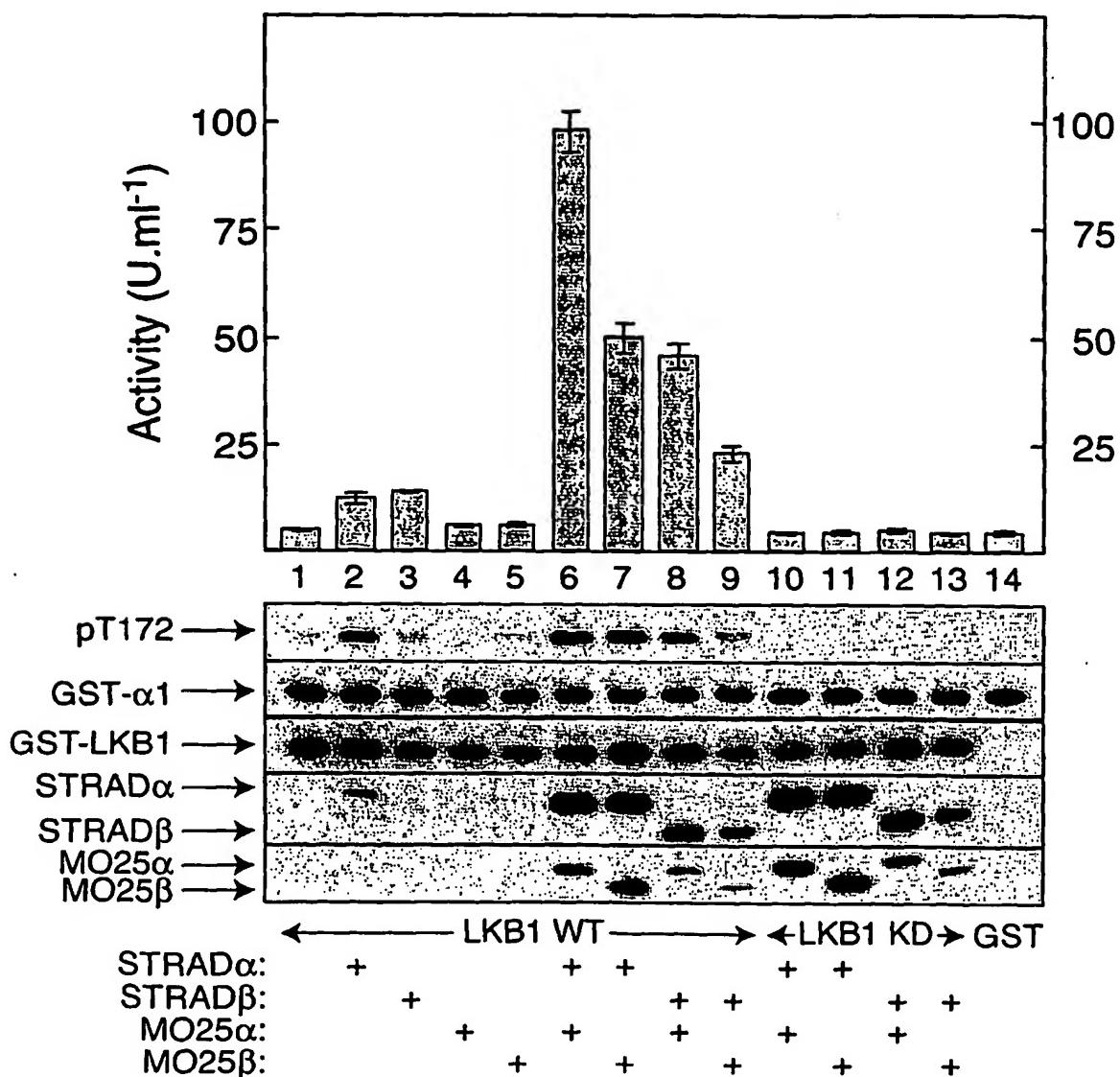
Figure 15**A) Activation of AMPK α 1 catalytic domain by LKB1**

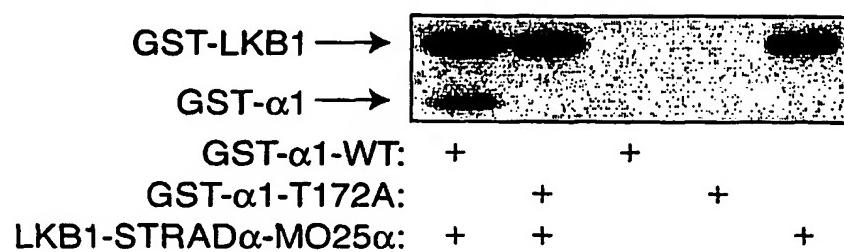
Figure 15a**B) Phosphorylation of AMPK α 1 catalytic domain by LKB1**

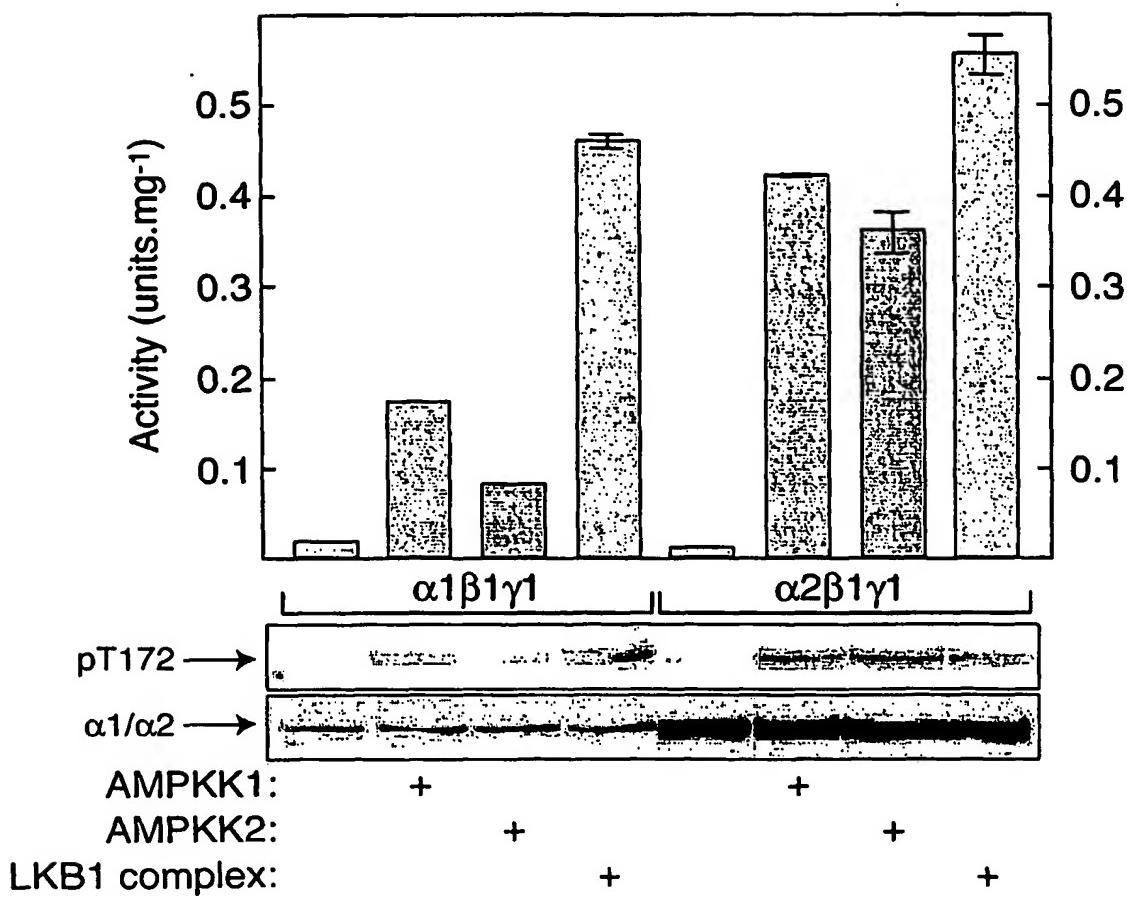
Figure 16

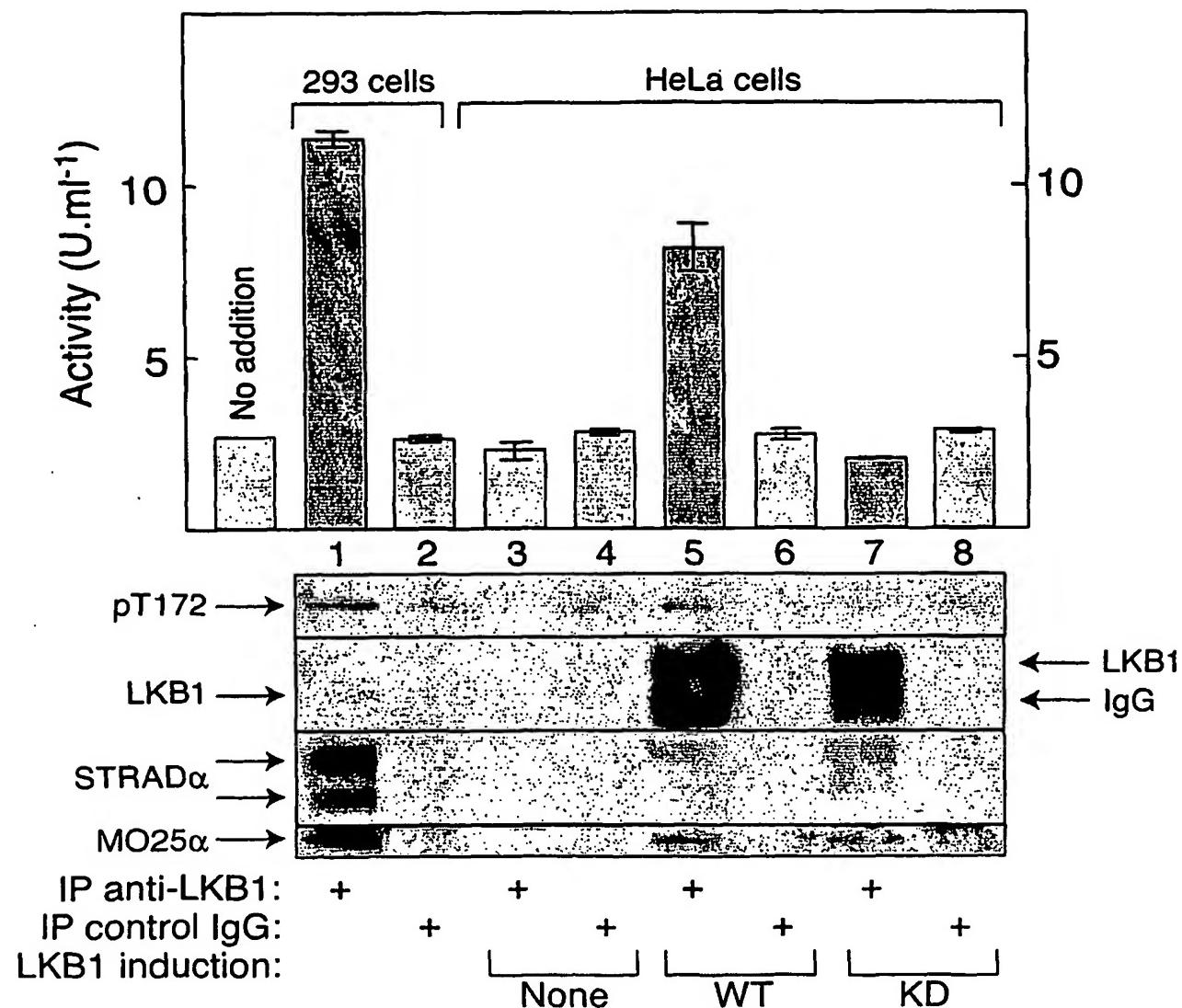
Figure 17

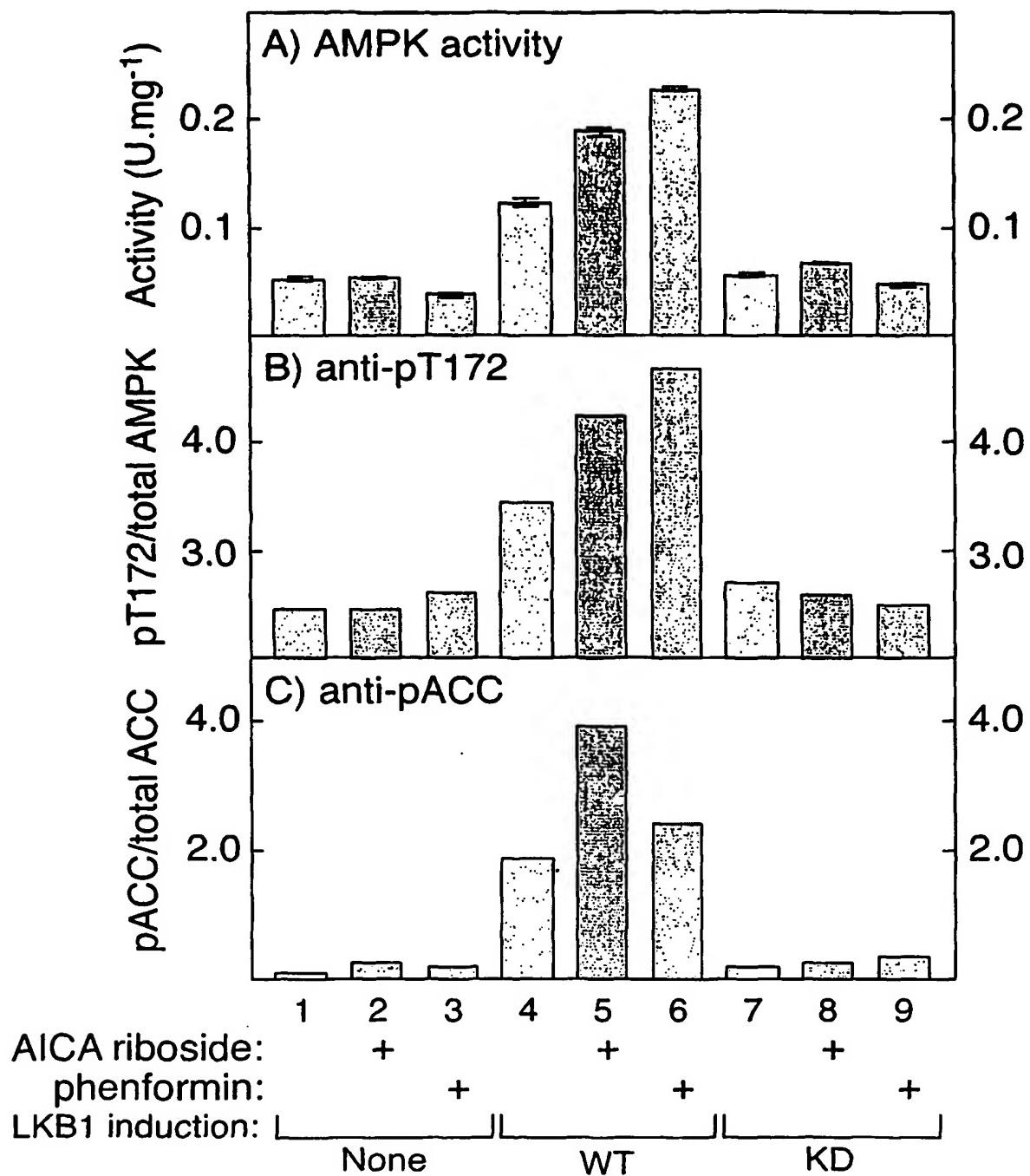
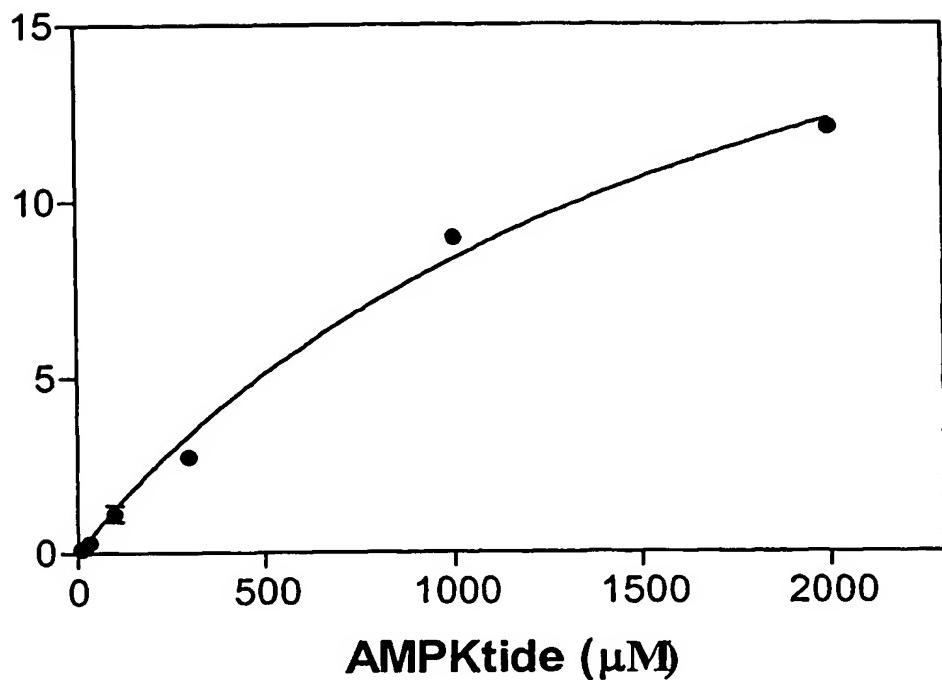
Figure 18

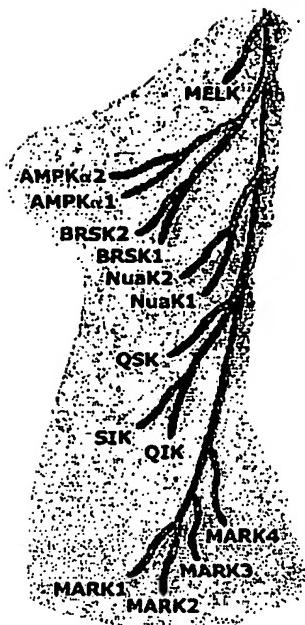
Figure 19

		-12	-11	-10-9	-5	-3 -2	P
PKA-C α	239	DFGFAKR..	V.KG.	RTWTLCGTPEYLAPE			
PKC α	539	DFGMCKEHMM.	DGVTRTRFCGT	PDYIAPE			
NuaK1	196	DFGLSNLYQKDK..	FLQTFCGSPLYASPE				
NuaK2	237	DFGLSNLYHQGK..	FLQTFCGSPLYASPE				
BrsK1	190	DFGMASLQVGDS..	LLETSCGSPHYACPE				
BrsK2	159	DFGMASLQVGDS..	LLETSCGSPHYACPE				
SIK	167	DFGFGNFYKSGE..	PLSTWCGSPPYAAPE				
QIK	160	DFGFGNFFKSGE..	LLATWCGSPPYAAPE				
AtSnRK1- α 1	160	DFGLSNIMRDGH..	FLKTSCGSPTYAAPE				
AtSnRK1- α 2	161	DFGLSNVMRDGH..	FLKTSCGSPTYAAPE				
AMPK- α 1	159	DFGLSNMMSDGE..	FLRTSCGSPTYAAPE				
AMPK- α 2	157	DFGLSNMMSDGE..	FLRTSCGSPTYAAPE				
ScSnf1	195	DFGLSNIMTDGN..	FLKTSCGSPTYAAPE				
QSK	206	DFGFSNLFTPQ..	LLKTWCGSPPYAAPE				
MELK	150	DFGLCAKPKGNDYHLQTCCGSLAYAAPE					
consensus	243	DFGlsnl	g	fL	TsCGSp	YAaPE	

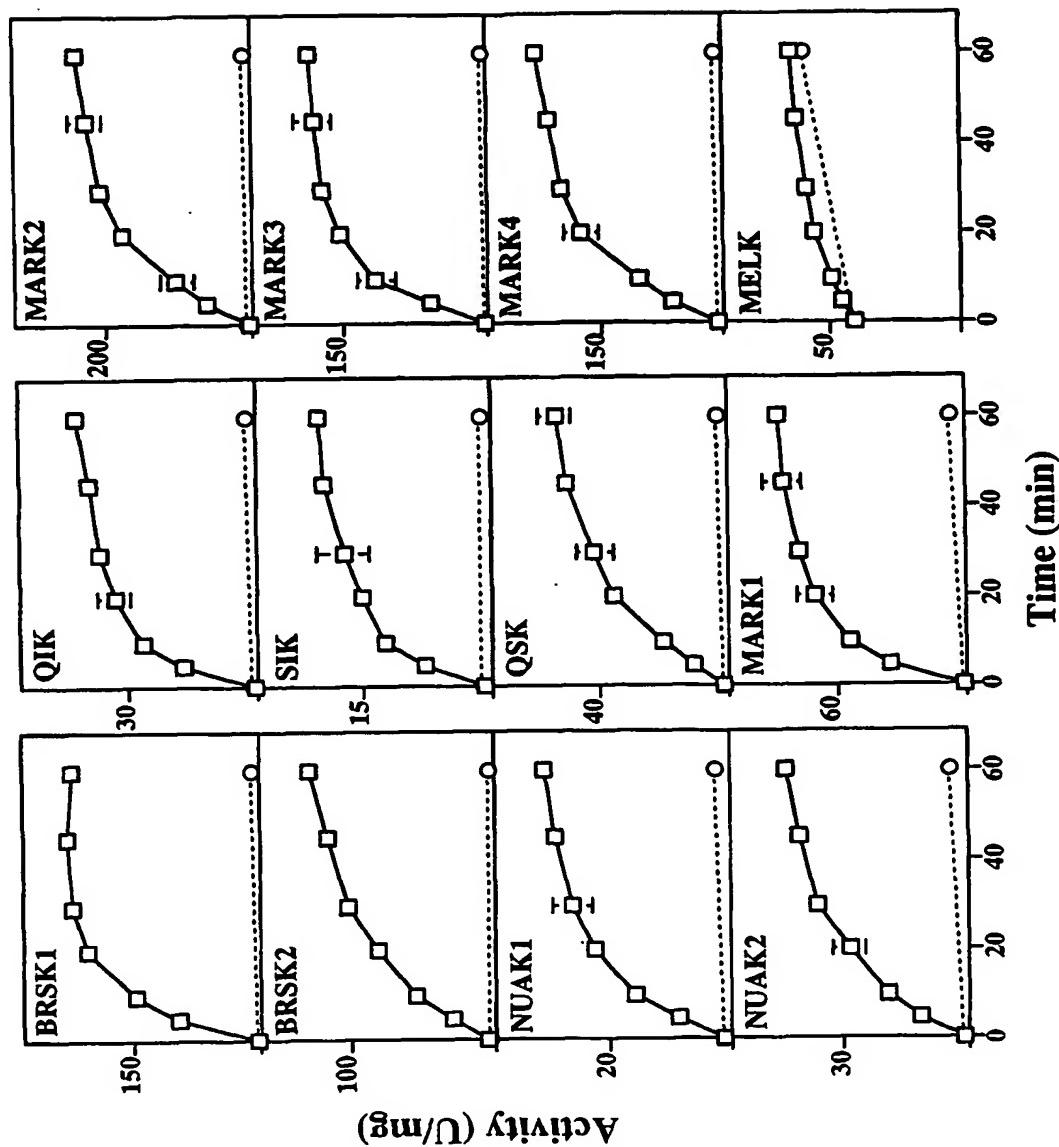
Figure 20

K_m: 1.80 ± 0.48

V_{max}: 23.43 ± 3.51 U/mg

Figure 21

AMPK1	159-	DFGLSNMMSDGE--FLRTSCGSPNYAAPE	*	*
AMPK2	157-	DFGLSNMMSDGE--FLRTSCGSPNYAAPE		
BRSK1	174-	DFGMASLQVGDS--LLETSCGSPHYACPE		
BRSK2	159-	DFGMASLQVGDS--LLETSCGSPHYACPE		
NUAK1	196-	DFGLSNLYQKDK--FLQTECGSPLYASPE		
NUAK2	193-	DFGLSNLYHQGK--FLQTECGSPLYASPE		
SIK	167-	DFGFGNFYKSGE--PLSTWCGSPPYAAPE		
QIK	160-	DFGFGNFFKSGE--LLATWCGSPPYAAPE		
QSK	206-	DFGFSNEFTPGQ--LLKTWCGSPPYAAPE		
MARK1	200-	DFGFSNEFTVGN--KLDTECGSPPYAAPE		
MARK2	160-	DFGFSNEFTVGN--KLDTECGSPPYAAPE		
MARK3	196-	DFGFSNEFTVGG--KLDTECGSPPYAAPE		
MARK4	198-	DFGFSNEFTLGS--KLDTECGSPPYAAPE		
MELK	150-	DFGLCAKPKGNKDYHLOTCGSLAYAAPE		

Figure 21A

30/38
Figure 22

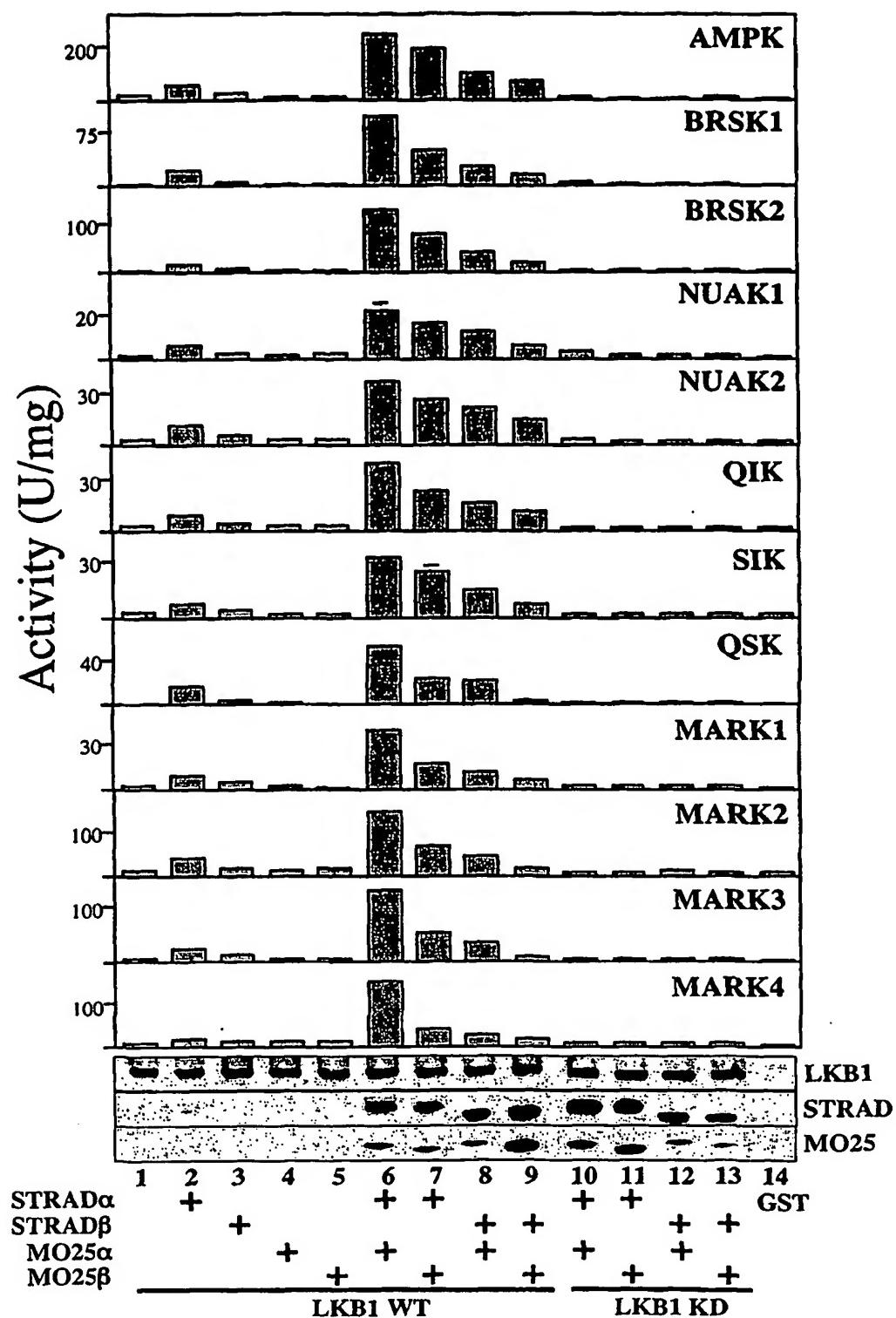


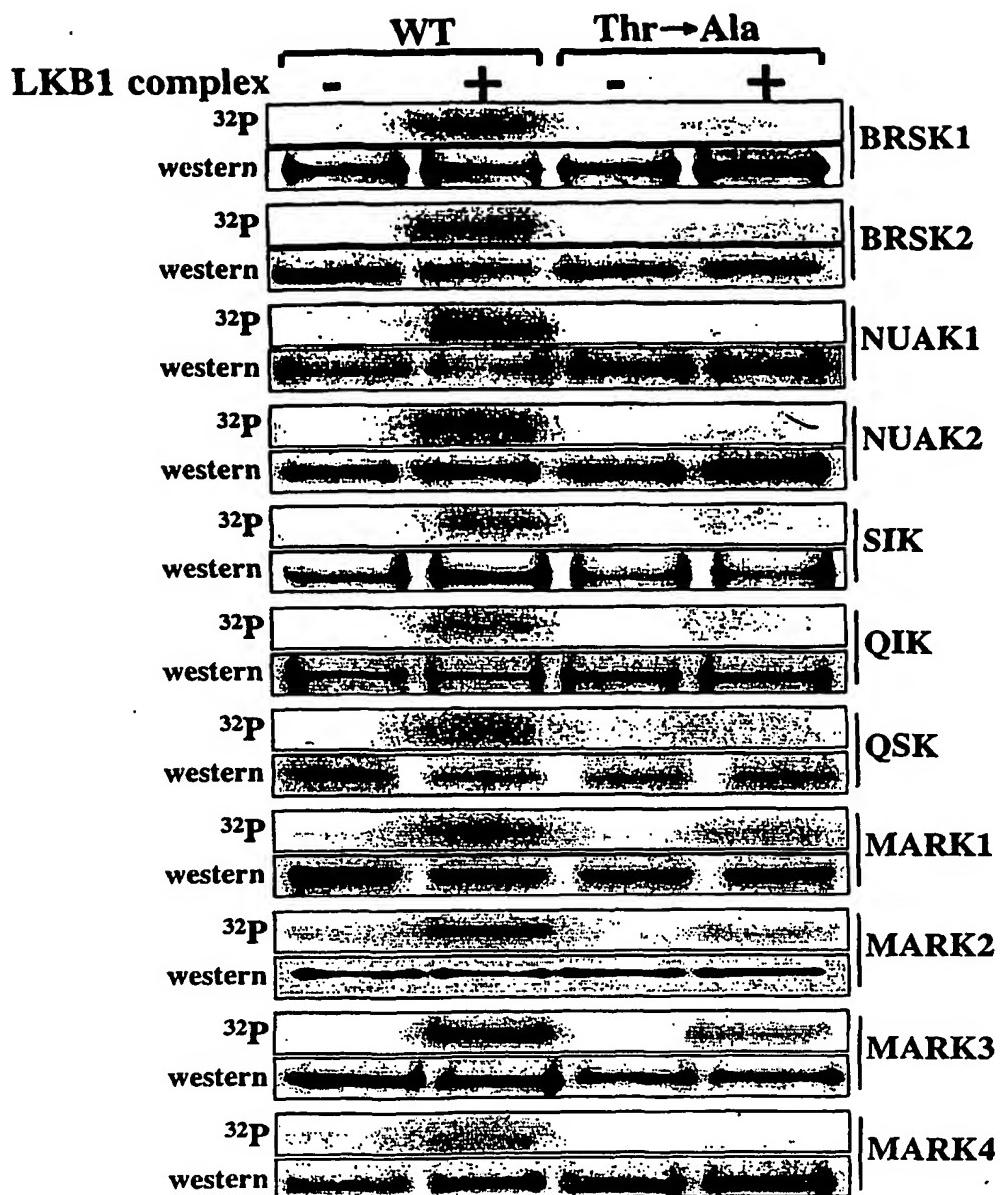
Figure 23

Figure 24

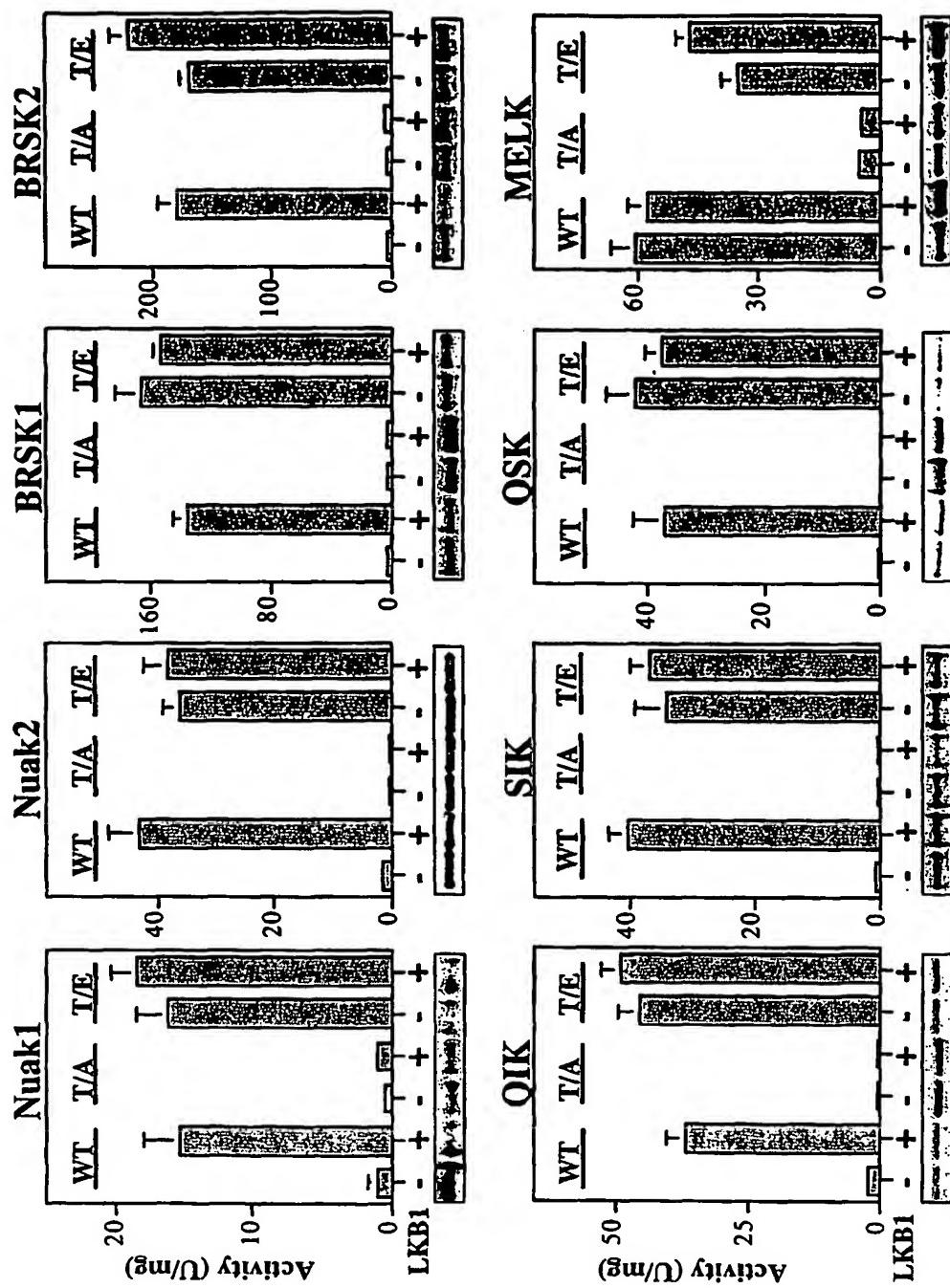


Figure 25

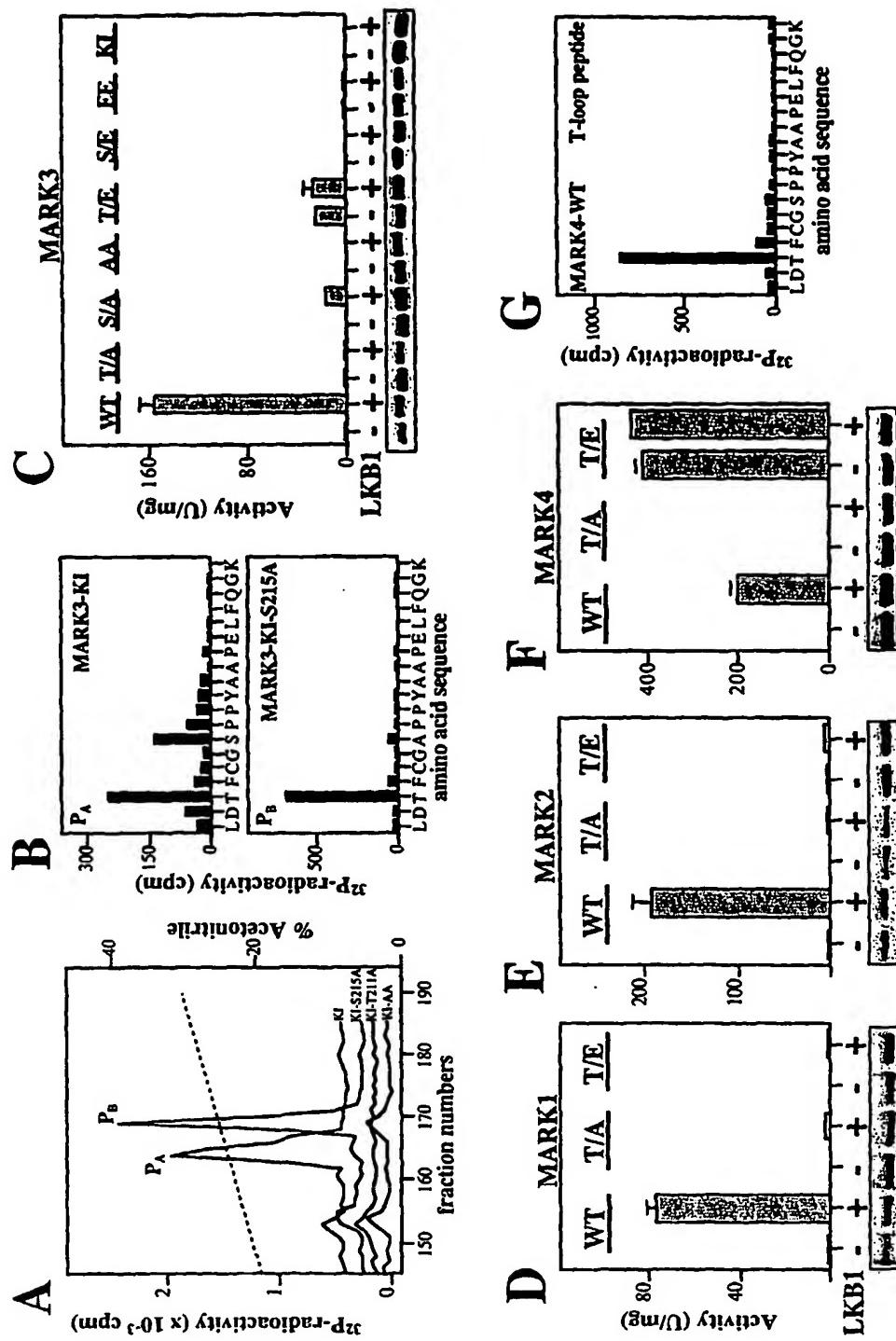


Figure 26

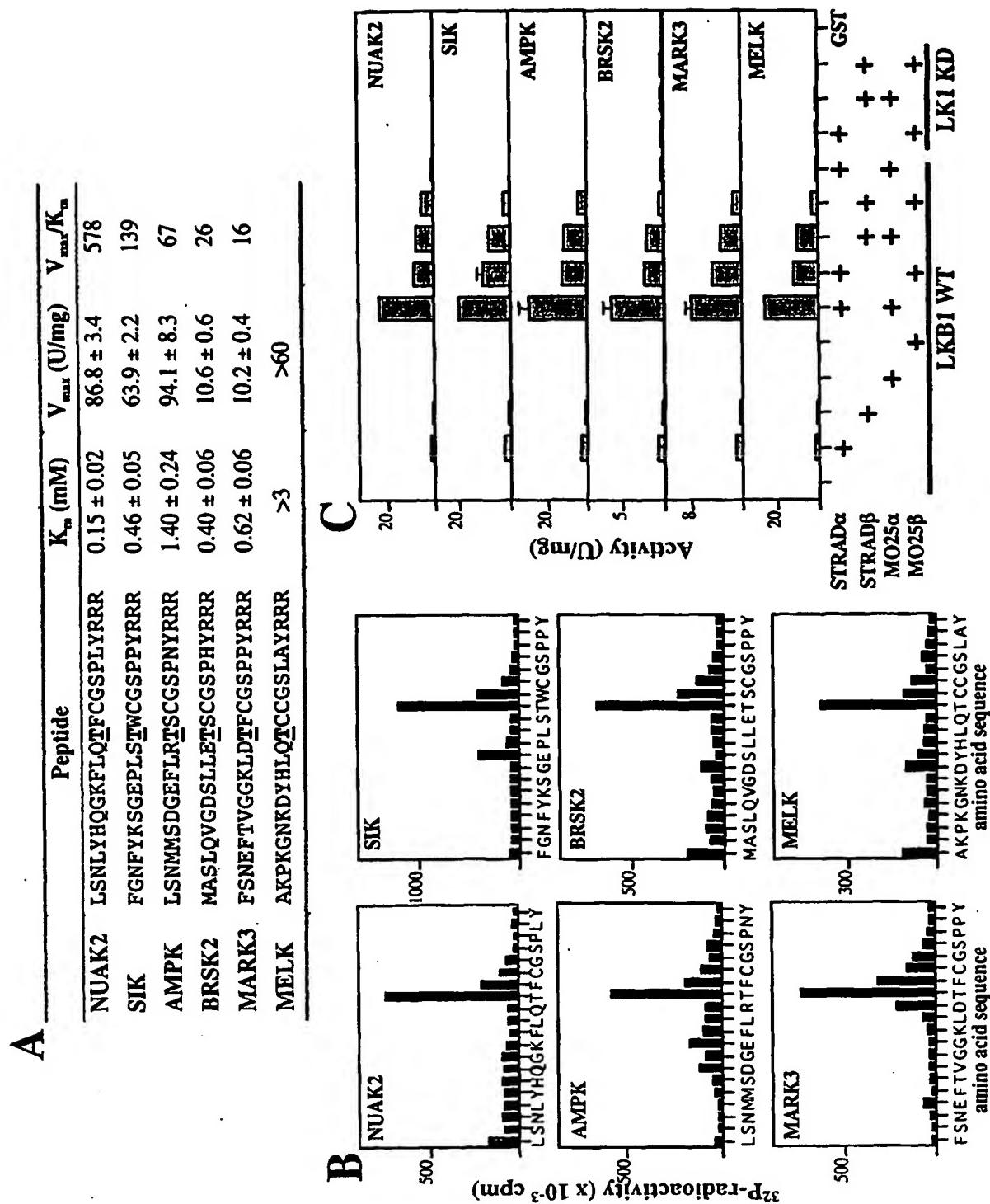


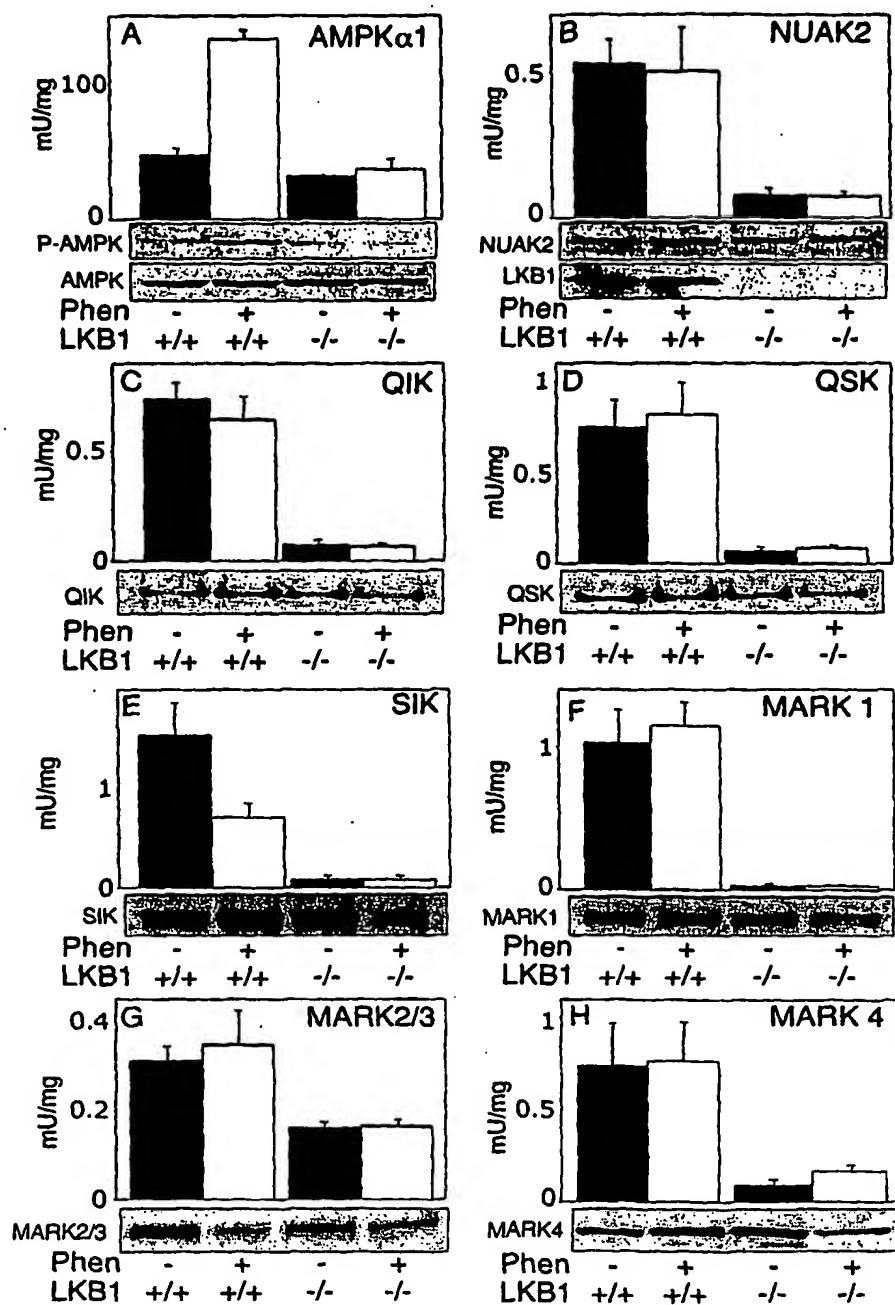
Figure 27

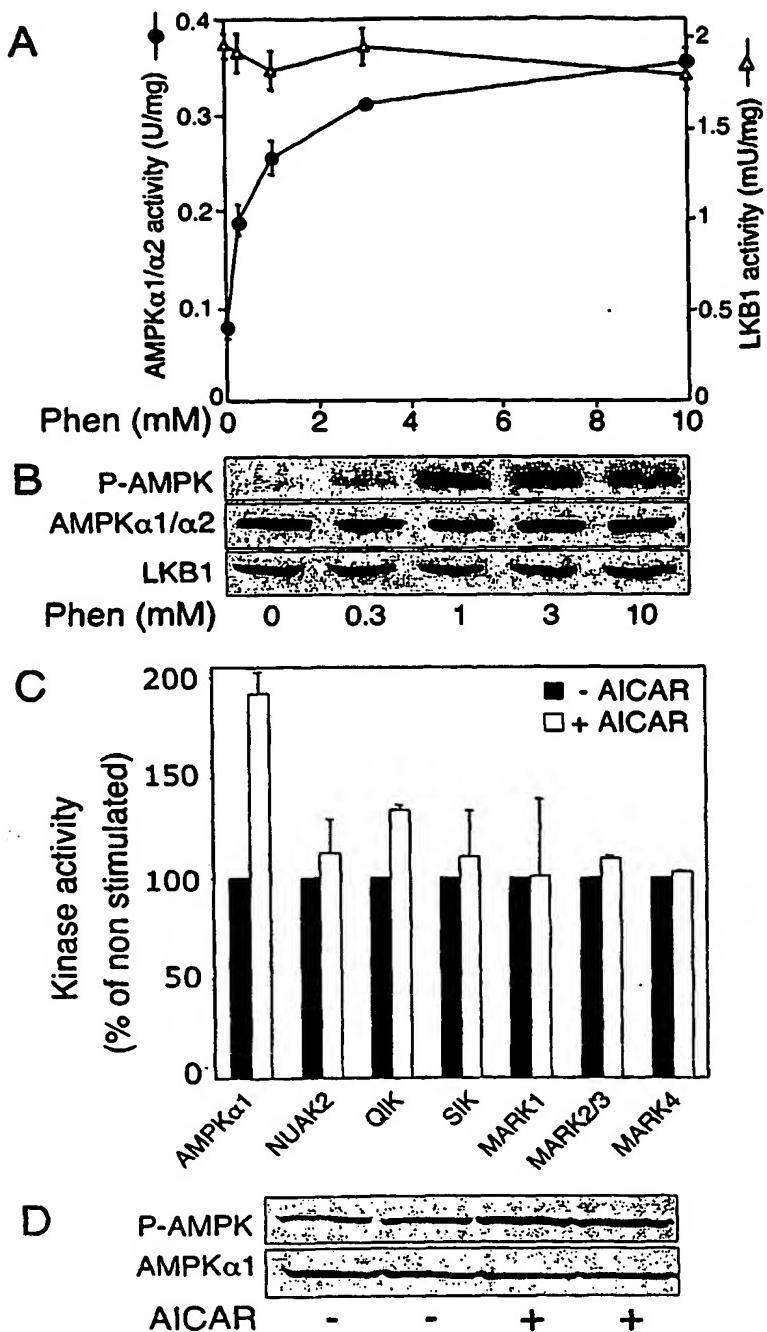
Figure 28

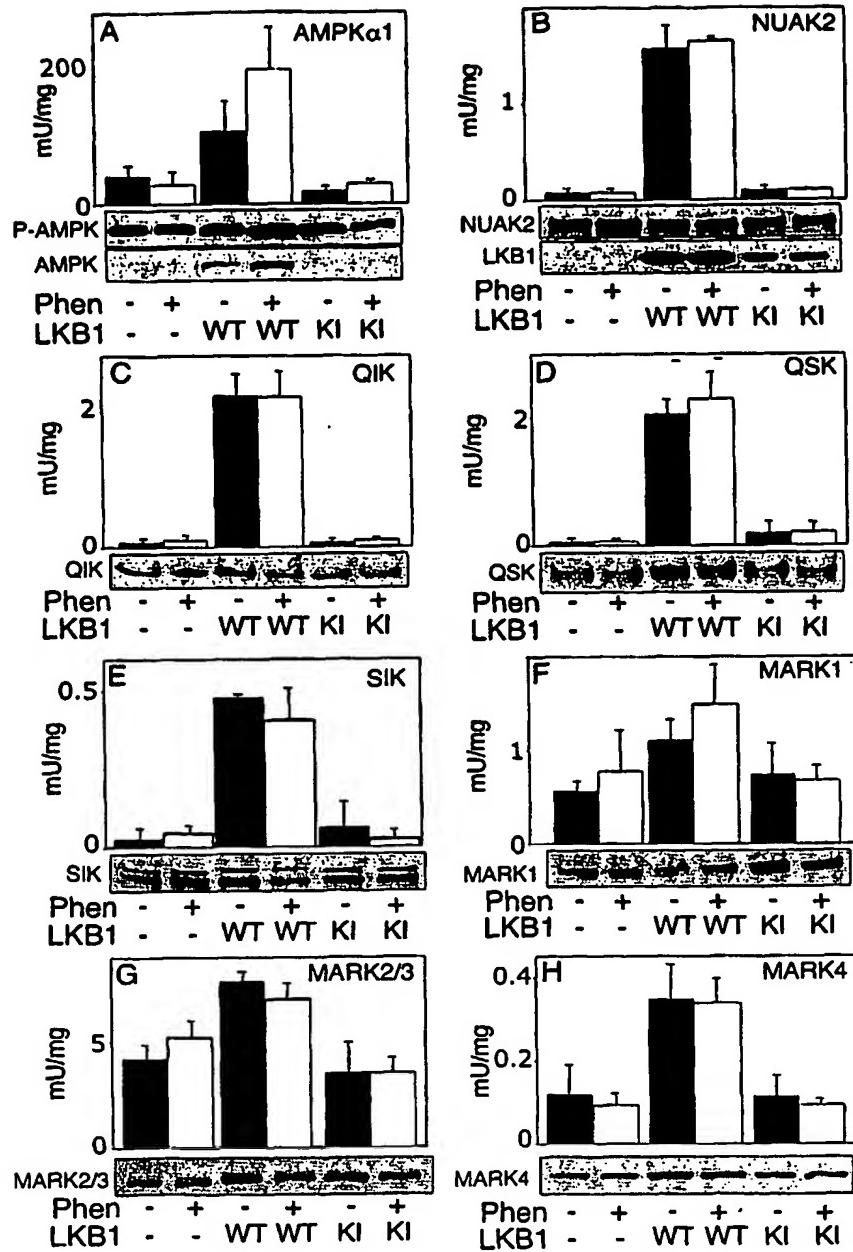
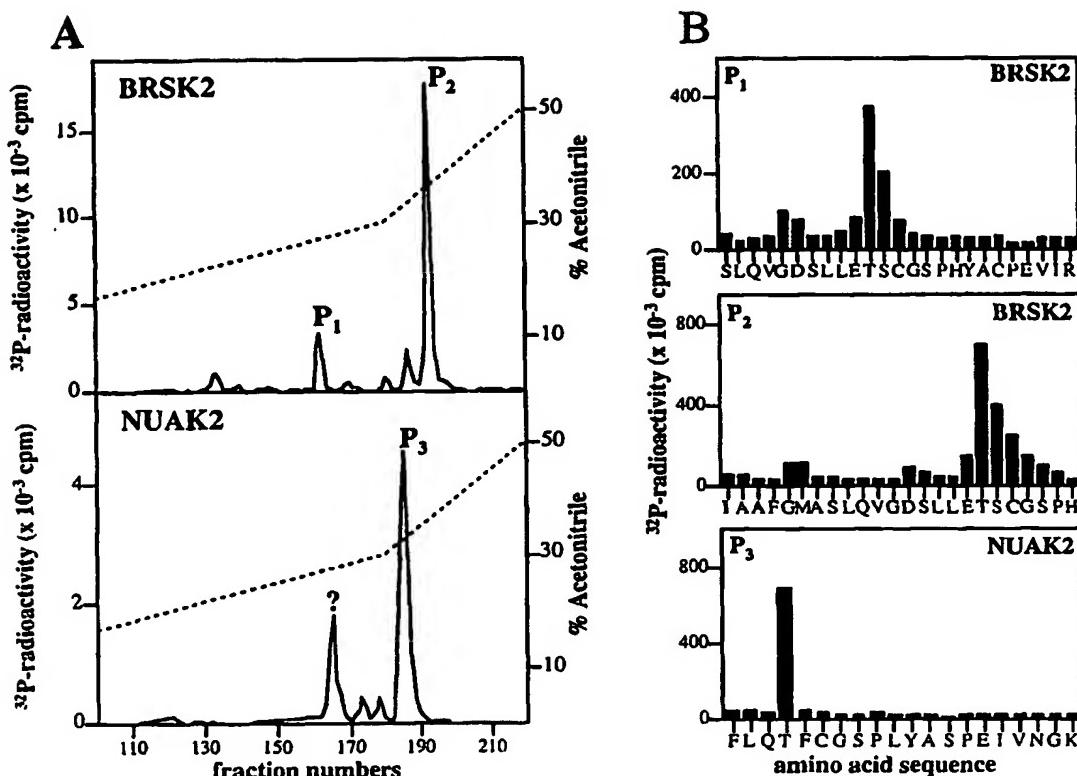
Figure 29

Figure 30

Kinase	Phosphopeptide	Mass observed	Theoretical mass
BRSK2 P ₁	IAAFGmASLQVGDSLLET(p)SCGSPHYACPEVIR	3268.7870	3628.6680
BRSK2 P ₂	SLQVGDSLLET(p)SCGSPHYACPEVIR	2951.4530	2951.3472
NUAK2 P ₃	FLQT(p)FCGSPLYASPEIVNGK	2356.1088	2356.1333
MARK4	LDT(p)FCGSPPYAAPELFQQK	2225.9983	2226.1497
MELK	GNKDYHLQT(p)CCGSLAYAAPELJQCK	2970.4421	2970.3648

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